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OM protein - protein search, using sw model

Run on: September 16, 2003, 18:10:03 : Search time 16 Seconds  
(without alignments)  
15,667 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35  
Sequence: 1 GRGTP 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4210858 residues

Total number of hits satisfying chosen parameters: 37639

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/aa/PCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	1	US-08-169-743-2
2	35	100.0	6	1	US-08-178-482-7
3	35	100.0	6	1	US-08-232-997-1
4	35	100.0	6	2	US-08-747-137-74
5	35	100.0	6	2	US-08-747-137-176
6	35	100.0	6	3	US-08-956-699-1
7	35	100.0	6	4	US-09-696-477-1
8	35	100.0	6	4	US-09-485-653-1
9	35	100.0	6	4	US-09-548-697A-2
10	35	100.0	6	5	PCT-US93-05640-45
11	31	88.6	6	1	US-07-729-222-46
12	31	88.6	6	1	US-07-780-790A-6
13	31	88.6	6	1	US-07-932-200-11
14	31	88.6	6	1	US-06-234-973-3
15	31	88.6	6	1	US-06-251-027-13
16	31	88.6	6	1	US-06-214-770-13
17	31	88.6	6	1	US-08-212-186A-2
18	31	88.6	6	1	US-08-169-743-4
19	31	88.6	6	1	US-08-262-315-1
20	31	88.6	6	1	US-08-425-238-7
21	31	88.6	6	1	US-08-178-482-6
22	31	88.6	6	1	US-08-264-759-3
23	31	88.6	6	1	US-08-445-745-49
24	31	88.6	6	1	US-08-608-697-1
25	31	88.6	6	1	US-08-596-116A-69
26	31	88.6	6	1	US-08-104-135-3
27	31	88.6	6	1	US-08-421-702A-4

28	31	88.6	6	1	US-08-482-105-16	Sequence 16, Appl
29	31	88.6	6	1	US-08-303-052A-4	Sequence 4, Appl
30	31	88.6	6	1	US-08-421-696A-4	Sequence 4, Appl
31	31	88.6	6	1	US-07-803-623H-12	Sequence 12, Appl
32	31	88.6	6	1	US-08-482-107B-3	Sequence 3, Appl
33	31	88.6	6	1	US-08-421-697A-4	Sequence 4, Appl
34	31	88.6	6	1	US-08-421-698A-4	Sequence 4, Appl
35	31	88.6	6	2	US-08-387-749-11	Sequence 11, Appl
36	31	88.6	6	2	US-08-520-535-15	Sequence 15, Appl
37	31	88.6	6	2	US-08-280-645-2	Sequence 2, Appl
38	31	88.6	6	2	US-08-445-193-2	Sequence 2, Appl
39	31	88.6	6	2	US-08-432-698-2	Sequence 2, Appl
40	31	88.6	6	2	US-08-635-572-1	Sequence 1, Appl
41	31	88.6	6	2	US-08-806-064-12	Sequence 12, Appl
42	31	88.6	6	2	US-08-421-695A-4	Sequence 4, Appl
43	31	88.6	6	2	US-08-473-025-3	Sequence 3, Appl
44	31	88.6	6	2	US-08-447-810-2	Sequence 2, Appl
45	31	88.6	6	2	US-08-585-281-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-169-743-2  
: Sequence 2, Application US/08169743  
: Patent No. 5547936  
: GENERAL INFORMATION:  
: APPLICANT: RUOSLAHTI, ERKKI  
: APPLICANT: PIERSBACHER, MICHAEL D.  
: APPLICANT: GEHLEN, KURT R.  
: TITLE OF INVENTION: INHIBITION OF CELL MIGRATION WITH  
: TITLE OF INVENTION: SYNTHETIC PEPTIDES  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
: STREET: 444 SOUTH FLOWER STREET, SUITE 2000  
: CITY: LOS ANGELES  
: STATE: CALIFORNIA  
: COUNTRY: UNITED STATES  
: ZIP: 90071  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/169,743  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/773,106  
: FILING DATE: 08-OCT-1992  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BROWN, THERESA A.  
: REGISTRATION NUMBER: 32,547  
: REFERENCE/DOCKET NUMBER: P419102  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 619-535-9001  
: TELEFAX: 619-535-8849  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 6 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
US-08-169-743-2

Query Match 100.0% Score 35: DB 1: Length 6:  
Best Local Similarity 100.0% Pred. No. 2.5e+05:  
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 1 GRGTP 6  
|||||

Db 1 GRGDTF 6

## RESULT 2

US-08-178-482-7  
 : Sequence 7, Application: US/08178482  
 : Patent No. 5629294  
 : GENERAL INFORMATION:  
 : APPLICANT: DIZERCA .. GERE S  
 : APPLICANT: ROGERS .. KATHLEEN E  
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTING  
 : TITLE OF INVENTION: ADHESION FORMATION  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: ROBBINS, DALGARIN, BERLINER & CARSON  
 : STREET: 201 NORTH FIGUEROA STREET, FIFTH FLOOR  
 : CITY: LOS ANGELES  
 : STATE: CALIFORNIA  
 : COUNTRY: USA  
 : ZIP: 90012-2628  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/178,482  
 : FILING DATE: 06-JAN-1994  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/789,231  
 : FILING DATE: 07-NOV-1991  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SPITALS .. JOHN P  
 : REGISTRATION NUMBER: 25,215  
 : REFERENCE/DOCKET NUMBER: 1920-314  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (213) 977-1001  
 : TELEFAX: (213) 977-1003  
 : INFORMATION FOR SEQ ID NO: 7:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 6 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : US-08-178-482-7

Query Match 100.0% Score 35; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6

Db 1 GRGDTF 6

## RESULT 3

US-08-234-997-1  
 : Sequence 1, Application: US/08234997  
 : Patent No. 5683867  
 : GENERAL INFORMATION:  
 : APPLICANT: SUMEDHA JAYASENA  
 : APPLICANT: GREG BIESECKER  
 : APPLICANT: LARRY GOLD  
 : APPLICANT: DREW SMITH  
 : APPLICANT: GARY KIRSCHENHEUTER  
 : TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
 : TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLENDED  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Beaton & Swanson, P.C.  
 : STREET: 4582 South Ulster Street Parkway, #403  
 : CITY: Denver

STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80237  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
 COMPUTER: IBM pc compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/234,997  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/714,131  
 FILING DATE: JUNE 10, 1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/536,428  
 FILING DATE: JUNE 11, 1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/117,991  
 FILING DATE: SEPTEMBER 8, 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/123,935  
 FILING DATE: SEPTEMBER 17, 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/199,507  
 FILING DATE: FEBRUARY 22, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 850-9900  
 TELEFAX: (303) 850-9401  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-234-997-1

Query Match 100.0% Score 35; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6

Db 1 GRGDTF 6

## RESULT 4

US-08-747-137-74  
 : Sequence 74, Application: US/08747137  
 : Patent No. 5945013  
 : GENERAL INFORMATION:  
 : APPLICANT: YEN, Richard C.K.  
 : TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
 : TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
 : NUMBER OF SEQUENCES: 184  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend and Crew LLP  
 : STREET: Two Embarcadero Center, 8th Floor  
 : CITY: San Francisco  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 94111  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:

```

1  APPLICATION NUMBER: US 08/747,137
2  FILING DATE: 12-NOV-1996
3  CLASSIFICATION: 424
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: US 08/212,546
6  FILING DATE: 14-MAR-1994
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: US 08/065,831
9  FILING DATE: 01-JUN-1993
10 APPLICATION DATA:
11 APPLICATION NUMBER: US 07/955,560
12 FILING DATE: 13-OCT-1992
13 APPLICATION DATA:
14 APPLICATION NUMBER: US 07/641,720
15 FILING DATE: 15-JAN-1991
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Apple, Randolph T.
18 REGISTRATION NUMBER: 36,429
19 REFERENCE/DOCKET NUMBER: 016197-0008400S
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 415-576-0200
22 INFORMATION FOR SEQ ID NO: 34:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 6 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: not relevant
27 TOPOLOGY: not relevant
28 US-08-747-137-74

```

```

Query Match 100.0% Score 35: DB 2: Length 6:
Best Local Similarity 100.0% Pred. No. 2.5e+05:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 GCGDTP 6
DB 1 GCGDTP 5

```

## RESULT 5

```

US-08-747-137-176
1 Sequence 176: Application US/08747137
2 Patent No. 5945033
3 GENERAL INFORMATION:
4 APPLICANT: YEN, Richard C.K.
5 TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
6 THERAPEUTIC AND DIAGNOSTIC USE
7 NUMBER OF SEQUENCES: 184
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Townsend and Townsend and Crew LLP
10 STREET: Two Embarcadero Center, 8th Floor
11 CITY: San Francisco
12 STATE: CA
13 COUNTRY: USA
14 ZIP: 94111
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: 5-copy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/747,137
22 FILING DATE: 12-NOV-1996
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/212,546
26 FILING DATE: 14-MAR-1994
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 08/065,831
29 FILING DATE: 01-JUN-1993
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/955,560
32 FILING DATE: 13-OCT-1992
33 PRIOR APPLICATION DATA:

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1  APPLICATION NUMBER: US 07/641,720
2  FILING DATE: 15-JAN-1991
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Apple, Randolph T.
5  REGISTRATION NUMBER: 36,429
6  REFERENCE/DOCKET NUMBER: 016197-0008400S
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: 415-576-0200
9  INFORMATION FOR SEQ ID NO: 176:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 6 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: not relevant
14 TOPOLOGY: not relevant
15 US-08-747-137-176

```

```

Query Match 100.0% Score 35: DB 2: Length 6:
Best Local Similarity 100.0% Pred. No. 2.5e+05:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GCGDTP 6
DB 1 GCGDTP 6

```

```

RESULT 6
US-08-956-699-1
1 Sequence 1: Application US/08956699
2 Patent No. 6083696
3 GENERAL INFORMATION:
4 APPLICANT: GREG BIESCHKE
5 APPLICANT: SUMEDHA D. JAYASENA
6 APPLICANT: LARRY GOLD
7 APPLICANT: DREW SMITH
8 APPLICANT: GARY P. KIRSCHENHEUTER
9 TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
10 TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLENDING
11 TITLE OF INVENTION: SELEX
12 NUMBER OF SEQUENCES: 5
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Swanson & Bratschan, L.L.C.
15 STREET: 8400 E. Prentice Avenue, Suite 100
16 CITY: Englewood
17 STATE: Colorado
18 COUNTRY: USA
19 ZIP: 80111
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: MS-DOS
24 SOFTWARE: WordPerfect 6.0
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/956,699
27 FILING DATE: OCTOBER 23, 1997
28 CLASSIFICATION: 435
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/234,997
31 FILING DATE: APRIL 28, 1994
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: 07/714,131
34 FILING DATE: JUNE 10, 1991
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: 07/536,428
37 FILING DATE: JUNE 11, 1990
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: 08/117,991
40 FILING DATE: SEPTEMBER 8, 1993
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: 08/123,935
43 FILING DATE: SEPTEMBER 17, 1993
44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: 08/199,507
46 FILING DATE: FEBRUARY 22, 1994

```

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Barry J. Swanson
3 REGISTRATION NUMBER: 33,215
4 REFERENCE/DOCKET NUMBER: NEX15/C
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (303) 793-3333
7 TELEFAX: (303) 793-3433
8 INFORMATION FOR SEQ ID NO: 1:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 6 amino acids
11 TYPE: amino acid
12 STRANDEDNESS: single
13 TOPOLOGY: linear
14
15 US-08-956-699-1
16
17 Query Match 100.0%; Score 35; DB 3; Length 6;
18 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
19 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20
21 QY 1 GRGDTF 6
22 DB 1 GRGDTF 6
23
24 RESULT 7
25 US-09-606-477-1
26 : Sequence 1, Application US/03606477
27 : Patent No. 6465189
28 : GENERAL INFORMATION:
29 : APPLICANT: GREG BIESECKER
30 : INVENTOR: LARRY GOLD
31 : DREW SMITH
32 : GARY P. KIRSCHENHEUTER
33 : TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
34 : EXPONENTIAL ENRICHMENT: BLENDSE
35 : SELEX
36 : NUMBER OF SEQUENCES: 5
37 : CORRESPONDENCE ADDRESS:
38 : ADDRESS: Swanson & Bratschan, L.L.C.
39 : STREET: 1745 Shea Center Drive, Suite 330
40 : CITY: Highlands Ranch
41 : STATE: Colorado
42 : COUNTRY: USA
43 : ZIP: 80129
44 : COMPUTER READABLE FORM:
45 : MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
46 : COMPUTER: IBM PC compatible
47 : OPERATING SYSTEM: MS-DOS
48 : SOFTWARE: WordPerfect 6.0
49 : CURRENT APPLICATION DATA:
50 : APPLICATION NUMBER: US/79/606,477
51 : FILING DATE: 29-Jun-2002
52 : CLASSIFICATION: <UNKNOWN>
53 : PRIOR APPLICATION DATA:
54 : APPLICATION NUMBER: 08/956,699
55 : FILING DATE: OCTOBER 23, 1997
56 : APPLICATION NUMBER: 08/234,997
57 : FILING DATE: APRIL 28, 1994
58 : APPLICATION NUMBER: 07/714,133
59 : FILING DATE: JUNE 10, 1991
60 : APPLICATION NUMBER: 07/536,428
61 : FILING DATE: JUNE 11, 1990
62 : APPLICATION NUMBER: 08/117,591
63 : FILING DATE: SEPTEMBER 8, 1993
64 : APPLICATION NUMBER: 08/123,935
65 : FILING DATE: SEPTEMBER 17, 1994
66 : APPLICATION NUMBER: 08/59,507
67 : FILING DATE: FEBRUARY 22, 1994
68 : ATTORNEY/AGENT INFORMATION:
69 : NAME: Barry J. Swanson
70 : REGISTRATION NUMBER: 33,215
71 : REFERENCE/DOCKET NUMBER: NEX15/C-CON

```

```

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (303) 793-3333
3 TELEFAX: (303) 793-3433
4 INFORMATION FOR SEQ ID NO: 1:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 6 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: single
9 TOPOLOGY: linear
10
11 US-09-606-477-1
12
13 Query Match 100.0%; Score 35; DB 4; Length 6;
14 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
15 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16
17 QY 1 GRGDTF 6
18 DB 1 GRGDTF 6
19
20 RESULT 8
21 US-09-485-653-1
22 : Sequence 1, Application US/09485653
23 : Patent No. 655321
24 : GENERAL INFORMATION:
25 : APPLICANT: Daniel, Thomas O.
26 : INVENTOR: STEIN, ELKE
27 : TITLE OF INVENTION: Methods for Determining Cell Responses
28 : THROUGH EPHRIN RECEPTORS
29 : FILE REFERENCE: 22000.008501
30 : CURRENT APPLICATION NUMBER: US/09/485,653
31 : PRIOR FILING DATE: 2000-02-14
32 : PRIOR APPLICATION NUMBER: PCT/US98/17157
33 : PRIOR FILING DATE: 1998-08-19
34 : PRIOR APPLICATION NUMBER: 60/056,164
35 : PRIOR FILING DATE: 1997-08-19
36 : NUMBER OF SEQ ID NOS: 3
37 : SOFTWARE: FastSeq for Windows Version 4.0
38 : SEQ ID NO 1
39 : LENGTH: 6
40 : TYPE: PRT
41 : ORGANISM: Artificial Sequence
42 : FEATURE:
43 : OTHER INFORMATION: Description of Artificial Sequence: No. 655321c -
44 : OTHER INFORMATION: Synthetic construct
45
46 US-09-485-653-1
47
48 Query Match 100.0%; Score 35; DB 4; Length 6;
49 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
50 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
51
52 QY 1 GRGDTF 6
53 DB 1 GRGDTF 6
54
55 RESULT 9
56 US-09-548-697A-2
57 : Sequence 2, Application US/09548697A
58 : Patent No. 6586187
59 : GENERAL INFORMATION:
60 : APPLICANT: American Cyanamid Company
61 : INVENTOR: Gopalsamy, Arimalla
62 : APPLICANT: Yang, Hui Y
63 : TITLE OF INVENTION: Methods for Solid Phase Combinatorial Synthesis of Integrin In
64 : FILE REFERENCE: AHP-98202
65 : CURRENT APPLICATION NUMBER: US/09/548,697A
66 : CURRENT FILING DATE: 2000-04-13
67 : PRIOR APPLICATION NUMBER: 60/240,952
68 : PRIOR FILING DATE: 1999-04-14
69 : NUMBER OF SEQ ID NOS: 9
70 : SOFTWARE: PatentIn version 3.1

```

SEQ ID NO 2  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: unknown  
 FEATURE:  
 OTHER INFORMATION: synthetic  
 US-09-548-697A-2

Query Match 100.0%; Score 35; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 GRGDT 6  
 Db 1 GRGDT 6

## RESULT 10

PCT-US93-05640-45  
 Sequence 45, Application PCT/US93/05640  
 GENERAL INFORMATION:  
 APPLICANT: University of Connecticut  
 TITLE OF INVENTION: Contraceptive Vaccine  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Million Drive  
 CITY: Lexington  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02173  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/05640  
 FILING DATE: 19930610  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/897,883  
 FILING DATE: June 12, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brook, David E.  
 REGISTRATION NUMBER: 22,592  
 REFERENCE/DOCKET NUMBER: UCT90-01AA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US93-05640-45

Query Match 100.0%; Score 35; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 GRGDT 6  
 Db 1 GRGDT 6

## RESULT 11

US-07-720-222-46  
 Sequence 46, Application US/07720222  
 Patent No. 5190873  
 GENERAL INFORMATION:

APPLICANT: Lernhardt, Waldemar  
 APPLICANT: Bourdon, Mario  
 APPLICANT: Youderian, Phil  
 TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bingham & Pitting  
 STREET: 11230 Sorrento Valley Road, Suite 200  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07720,222  
 FILING DATE: 19910621  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bingham, Douglas A.  
 REGISTRATION NUMBER: 32,457  
 REFERENCE/DOCKET NUMBER: C180612P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-587-3533  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-07-720-222-46

Query Match 88.8%; Score 31; DB 1; Length 5;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+5;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 GRGDT 6  
 Db 1 GRGDT 6

## RESULT 12

US-07-780-790A-6  
 Sequence 6, Application US/07780790A  
 Patent No. 5298488  
 GENERAL INFORMATION:  
 APPLICANT: KOJIMA, Masayoshi  
 APPLICANT: KOMAZAWA, Hiroyuki  
 TITLE OF INVENTION: CN-CHITIN DERIVATIVES AND USE THEREOF  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sughrue, Mior, Zinn, Macpeak, & Seas  
 STREET: 2100 Pennsylvania Avenue  
 CITY: Washington  
 STATE: District of Columbia  
 COUNTRY: USA  
 ZIP: 20037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07780,790A  
 FILING DATE: 1991023  
 CLASSIFICATION: 530

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060  
 TELEFAX: (202)293-7860  
 TELEX: 6491103

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-07-780-790A-6

Query Match 88.6%; Score 31; DB 1; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 GRGDTP 6  
 Db 1 GRGDSP 6

## RESULT 13

US-07-932-200-11

Sequence 11, Application US/07932200

Patent No. 5366862

## GENERAL INFORMATION:

APPLICANT: VENTON, DUANE L.  
 APPLICANT: HOPFINGER, ANTON J.

APPLICANT: LE BRETON, GUY

TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
 NUMBER OF SEQUENCES: 20

## CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 SEVENTH STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/932,200

FILING DATE: 21-AUG-1992

CLASSIFICATION: 4.5

## ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: VENTON-11

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

## INFORMATION FOR SEQ ID NO: 11:

## SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-932-200-11

Query Match 88.6%; Score 31; DB 1; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 GRGDTP 6  
 Db 1 GRGDSP 6

## RESULT 14

US-08-234-979-3

Sequence 3, Application US/08234979

Patent No. 5510328

## GENERAL INFORMATION:

APPLICANT: Schreiber, Ronda

APPLICANT: Polarek, James

APPLICANT: Tamura, Richard

APPLICANT: Harper, John

TITLE OF INVENTION: Compositions that inhibit wound

contraction and methods of using same

NUMBER OF SEQUENCES: 5

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,979

FILING DATE: 28-APR-1994

CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-1A 9955

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9900

TELEFAX: (619) 535-8949

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-234-979-3

Query Match 88.6%; Score 31; DB 1; Length 6;

Best Local Similarity 83.3%; Pred. No. 2.5e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 GRGDTP 6

Db 1 GRGDSP 6

## RESULT 15

US-08-251-027-13

Sequence 13, Application US/08251027

Patent No. 5519005

## GENERAL INFORMATION:

APPLICANT: Lider, Ofer

APPLICANT: Greenspoon, No. 5519005a

APPLICANT: Hershkoviz, Rami

APPLICANT: Alon, Ronen

TITLE OF INVENTION: A METHOD OF INHIBITION OF CELLULAR AND

MOLECULAR LEVEL BIOLOGICAL INTERACTIONS UTILIZING

NON-PEPTIDIC SURROGATES OF THE ARG-GLY-ASP SEQUENCE

NUMBER OF SEQUENCES: 16

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Kohn &amp; Associates

STREET: 30500 No. 5519005thwestern Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

QY 1 GRGDTP 6  
 Db 1 GRGDSP 6

1 COMPUTER READABLE FORM:  
2 MEDIUM TYPE: Floppy disk  
3 COMPUTER: IBM PC compatible  
4 OPERATING SYSTEM: PC-DOS/MS-DOS  
5 SOFTWARE: Patent In Release #1.0, Version #1.30  
6 CURRENT APPLICATION DATA:  
7 APPLICATION NUMBER: US/28/251,627  
8 FILING DATE:  
9 CLASSIFICATION: 514  
10 ATTORNEY/AGENT INFORMATION:  
11 NAME: Koho, Kenneth I.  
12 REGISTRATION NUMBER: 30,955  
13 TELECOMMUNICATION INFORMATION:  
14 TELEPHONE: (810) 539-5950  
15 TELEFAX: (810) 539-5055  
16 INFORMATION FOR SEQ ID NO: 13:  
17 SEQUENCE CHARACTERISTICS:  
18 LENGTH: 6 amino acids  
19 TYPE: amino acid  
20 STRANDEDNESS: single  
21 TOPOLOGY: linear  
22 MOLECULE TYPE: peptide  
23 US-08-251-027-13

Query Match 88.6% Score 41 DB 17 Length 6  
Best Local Similarity 83.3% Prod. No. 2.5e-05  
Matches 5: Conservative 1: Mismatches 0: Gaps 0:

QY 1 GRGUTP 6

DB 1 GRGDSP 6

Search completed: September 16, 2003, 16:21:21  
Job time : 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 16:17:03 : Search time 38 seconds  
(without alignments)  
25.062 Million cell updates/sec

Title: US-09-780-612A-1  
Perfect score: 35  
Sequence: 1 GRG5P 6

Scoring table: BLASTJ62  
Gapop 10.0 : Gapext 0.5

Searched: 1:07563 seqs, 158726574 residues

Total number of hits satisfying chosen parameters: 50962

Minimum DB seq length: 6  
Maximum DB seq length: 6

Post-processing: Minimum Match: 0%  
Maximum Match: 100%  
Listing first 45 summaries

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23: /SIDSL/qcqdqata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL/qcqdqata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	14	Adhesion formation
2	35	100.0	6	15	PA-30 beta disintegrin
3	35	100.0	6	17	Synthetic protein
4	35	100.0	6	17	RGD peptide, Syst
5	35	100.0	6	20	Neurogenin-1, activat
6	35	100.0	6	20	Non-crosslinked pr
7	35	100.0	6	20	Non-crosslinked pr
8	35	100.0	6	20	RGD peptide that s
9	35	100.0	6	2:	Peptide #3 used to

10	35	100.0	6	21	AA190475	Cell adhesion pept
11	35	100.0	6	22	AA191972	Fibronectin fragme
12	35	100.0	6	23	ABB80076	Integrin modulator
13	31	88.6	6	11	AA190461	Antiviral agent
14	31	88.6	6	11	AA190645	Fibronectin derivate
15	31	88.6	6	13	AA192908	Peptide contg. RGD
16	31	88.6	6	13	AA192908	Peptide contg. RGD
17	31	88.6	6	13	AA192908	Peptide lipid cont
18	31	88.6	6	13	AA192908	Peptide lipid cont
19	31	88.6	6	13	AA192908	Peptide contg. RGD
20	31	88.6	6	13	AA192908	Peptide contg. RGD
21	31	88.6	6	13	AA192908	Peptide contg. RGD
22	31	88.6	6	13	AA192908	Peptide contg. RGD
23	31	88.6	6	13	AA192908	Peptide contg. RGD
24	31	88.6	6	13	AA192908	Peptide contg. RGD
25	31	88.6	6	13	AA192908	Peptide contg. RGD
26	31	88.6	6	13	AA192908	Peptide contg. RGD
27	31	88.6	6	13	AA192908	Peptide contg. RGD
28	31	88.6	6	13	AA192908	Peptide contg. RGD
29	31	88.6	6	13	AA192908	Peptide contg. RGD
30	31	88.6	6	13	AA192908	Peptide contg. RGD
31	31	88.6	6	13	AA192908	Peptide contg. RGD
32	31	88.6	6	13	AA192908	Peptide contg. RGD
33	31	88.6	6	13	AA192908	Peptide contg. RGD
34	31	88.6	6	13	AA192908	Peptide contg. RGD
35	31	88.6	6	13	AA192908	Peptide contg. RGD
36	31	88.6	6	13	AA192908	Peptide contg. RGD
37	31	88.6	6	13	AA192908	Peptide contg. RGD
38	31	88.6	6	13	AA192908	Peptide contg. RGD
39	31	88.6	6	13	AA192908	Peptide contg. RGD
40	31	88.6	6	13	AA192908	Peptide contg. RGD
41	31	88.6	6	13	AA192908	Peptide contg. RGD
42	31	88.6	6	13	AA192908	Peptide contg. RGD
43	31	88.6	6	13	AA192908	Peptide contg. RGD
44	31	88.6	6	13	AA192908	Peptide contg. RGD
45	31	88.6	6	13	AA192908	Peptide contg. RGD

## ALIGNMENTS

PEP11: 1  
AA1936709  
10 AAR36709 standard; peptide; 6 AA.  
AC  
AA1936709:  
XX  
L1 25-MAR-2003 (updated)  
DT 26-AUG-1993 (first entry)  
DE Adhesion formation prevention RGD-contg. peptide.  
XX  
XX Tissue repair; peritoneum; surgery; post-surgically; inhibition;  
XX platelet aggregation; cardiovascular; orthopedic; thoracic;  
XX ophthalmic; CNS; use.  
XX Synthetic.  
XX  
XX W09308818-A1.  
XX  
XX 13-MAY-1993.  
XX  
XX 06-NOV-1992; 92WO-US05494.  
XX  
XX 07-NOV-1991; 91US-0789231.  
XX  
XX (USPTO) UNIV SOUTHERN CALIFORNIA.  
XX  
XX Bizerrega GS, Rodgers KE;  
XX WPI; 1993-167381/20.  
XX  
XX Prevention of adhesion formation, partic. post-surgically - comprises



PT administering a RGD-contg. peptide for a time sufficient to permit  
tissue repair

Example: Page 18; 22pp; English.

The sequence is that of an RGD-contg. peptide which is used in a  
method for prevention of adhesion formation for a time sufficient  
to permit tissue repair. The method is used for minimising or  
preventing adhesion formation, partic. in the peritoneum following  
surgery, but also for e.g. cardiovascular, orthopedic, thoracic,  
ophthalmic, CNS and other uses. In addn., the peptide inhibits  
platelet aggregation and does not induce inflammation or trauma  
at the site of administration.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDTP 6  
IIIII

DB 1 GRGDTP 6

RESULT 2

AAAR47384  
ID AAR47384 standard; Protein: 6 AA.

XX AC AAR47384;

XX DT 25-MAR-2003 (updated)

XX DT 22-JUN-1994 (first entry)

DE PH-30 beta disintegrin control peptide.

XX PH-20; PH-30; contraceptive; fertilisation; sperm surface protein;  
KW vaccine; sperm-egg fusion.

XX OS Rubella virus.

XX PN WO9325233-A1.

XX PD 23-DEC-1993.

XX PF 10-JUN-1993; 93WO-US05640.

XX PR 12-JUN-1992; 92US-0897983.

XX PA (UYCO-) UNIV CONNECTICUT.

XX PI Myles DG, Primakoff P;

XX PR WPI; 1994-007200/01.

XX PT Contraceptive vaccine for reducing sperm-egg fusion - comprises  
PT peptide from sperm surface protein which stimulates antibody  
PT prodn.

XX Example 7; Page 27; 79pp; English.

XX CC Example 7 describes the use of PH-30 beta disintegrin peptides  
CC as inhibitors of sperm fusion to egg plasma membrane.  
CC CC Modified peptides AAR47382-83 and control peptides (AAR47384-85)  
CC were tested. From observations it was concluded that the  
CC PH-30 beta disintegrin domain represents an epitope which  
CC is critical in sperm-egg fusion.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 15; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDTP 6  
IIIII

DB 1 GRGDTP 6

RESULT 3

AAAR07430  
ID AAR07430 standard; peptide: 6 AA.

XX AC AAR07430;

XX DT 25-MAR-2003 (updated)

XX DT 21-JAN-1997 (first entry)

XX DE Synthetic, preferred tumour invasion-inhibitory peptide.

XX KW Tumour invasion; extracellular matrix; ECM; metastasis; RGD sequence;  
XX cancer; inhibition; control.

XX OS Synthetic.

XX PR US5547936-A.

XX PD 20-AUG-1996.

XX PF 17-DEC-1993; 93US-0169743.

XX PR 17-DEC-1993; 93US-0169743.

XX PR 22-NOV-1983; 83US-0554821.

XX PR 17-JUN-1985; 85US-0744981.

XX PR 10-MAR-1988; 88US-0166530.

XX PR 09-SEP-1988; 88US-0242713.

XX PR 25-FEB-1991; 91US-0660526.

XX PR 10-APR-1991; 91US-0883585.

XX PR 08-OCT-1991; 91US-0773106.

XX PR 19-JUN-1992; 92US-0902742.

XX PA (JCOL-) LA JOLLA CANCER RES FOUND.

XX PR Gehlsen KR, Pierschbacher MD, Ruoslahti E;

XX WPI; 1996-392651/39.

XX PT Inhibiting tumour cell invasion through an extracellular matrix -  
PT using peptide contg. the RGD sequence, partic. for preventing tumour  
PT metastasis

XX Claim 2; Column 7-8; 8pp; English.

XX CC AAR07430 is a preferred peptide identified in an assay for testing  
CC peptides for tumour-invasion inhibitory activity. The peptides  
CC (contg. the RGD sequence) shows significant inhibition of tumour  
CC invasion of the ECM. Other peptides tested (see AAR07431-W06433) did  
CC show inhibitory activity but to a lesser extent than peptide AAR07430  
CC The peptides identified can be used to treat cancer and to prevent  
CC metastasis, in partic. invasion of the extracellular matrix (ECM).  
CC The peptides are soluble.  
CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDTP 6  
IIIII

DB 1 GRGDTP 6

RESULT 4  
AAR94571  
ID AAR94571 standard; Peptide: 6 AA.  
XX AC AAR94571:  
XX  
DT 21-JUN-1996 (first entry)  
DE RGD peptide.  
XX Cytotactin; neuron; neurite; cell attachment; cell elongation;  
KW antibody.  
XX Synthetic.  
XX W09608513-A1.  
XX  
PD 21-MAR-1996.  
XX  
PF 14-SEP-1995; 95W0-051164.  
XX  
PR 16-SEP-1994; 94US-0306359.  
XX  
FA (SCRI ) SCRIPPS RES INST.  
PI Crossin KL, Phillips G, Prieto AL  
DR WPI; 1996-179904/18.  
XX Cytotactin polypeptide(s), derivs. and antibodies - capable of  
PT stimulating neuronal cell attachment; neurite outgrowth and cell  
PT elongation  
XX  
PS Example 5; Page 82; 159pp; English.  
XX  
CC RGD peptides (AAR94570 and AAR94571), inhibitors of cell attachment to  
CC type I collagen, inhibited attachment of chicken fibroblasts to  
CC cytotactin (see also AAR94547-48) by 73% and 70% respectively.  
CC Inhibition was total when the peptides were used together with RGD2.  
CC A function-blocking monoclonal antibody against the beta-1 integrin.  
CC This suggests that there are 2 integrin binding sites on cytotactin.  
XX  
SQ Sequence 6 AA:  
Query Match 100.0%; Score 35; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GRGDTTP 6  
DB 1 GRGDTTP 6  
RESULT 5  
AAY50314  
ID AAY50314 standard; Peptide: 6 AA.  
XX AC AAY50314:  
XX  
DT 12-JAN-2000 (first entry)  
DE Neutrophil-activating pancreatic derived peptide i14.  
XX  
KW Cell activation; pancreas; treatment; cardiovascular disease; trauma;  
KW inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke;  
KW organ rejection; ischemia; Alzheimer's disease; myocardial infarction;  
KW haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina;  
KW trauma; protease inhibitor; hypertension; sepsis.  
XX  
OS Unidentified.  
XX  
PN W059946367-A2.  
XX

PD 16-SEP-1999.  
XX  
PF 11-MAR-1999; 99W0-US05247.  
XX  
PR 11-MAR-1998; 98US-0038654.  
XX  
PA (CELL-) CELL ACTIVATION INC.  
PA (REGC ) UNIV CALIFORNIA.  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;  
XX  
WK WPI; 1999-580234/49.  
XX  
XX Use of cell activating compositions in developing products for  
PI diagnosis and treatment of e.g. cardiovascular, inflammatory,  
PT autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,  
PI diabetes, stroke or ischemia.  
XX  
PS Example 9; Page 164; 164pp; English.  
XX  
CC This invention describes a novel method for the use and preparation of  
CC cell activating compositions which involves preparing a cell activating  
CC composition comprising (a) homogenizing pancreatic tissue in buffer at  
CC about neutral or higher pH to produce a homogenate; (b) removing  
CC particulates from the homogenate; (c) optionally incubating the  
CC resulting homogenate, with particulates removed with a protease; and  
CC (d) fractionating the homogenate and selecting fractions that exhibit  
CC cell activation activity. The methods can be used for improving  
CC treatment outcome or reducing risk of treatment of e.g. cardiovascular  
CC disease, inflammatory disease, trauma, autoimmune diseases, arthritis,  
CC organ rejection, diabetes and diabetic complications, stroke, ischemia,  
CC Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic  
CC retinopathy, diabetes, venous insufficiency, unstable angina or trauma.  
CC They can be used in the veterinary treatment of a non-human subject.  
CC Protease inhibitors can be used to lower cell activation resulting from  
CC these diseases and deficiencies. The detection of an elevated level of  
CC hydrogen peroxide can be used to detect an inflammatory condition. An  
CC elevated level of hydrogen peroxide in plasma or whole blood and in the  
CC presence of superoxide dismutase (SOD) indicates leukocyte up  
CC regulation, e.g. indicative of the onset of an acute cardiovascular  
CC disorders, such as disease onset or ischemic complications. An elevated  
CC level of hydrogen peroxide in plasma or whole blood and a low level in  
CC the presence of SOD is indicative of a chronic or immune compromised  
CC condition e.g. hypertension or sepsis. AAY50201-V50334 represent peptides  
CC used in the method of the invention.  
XX  
SQ Sequence 6 AA:  
Query Match 100.0%; Score 35; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GRGDTTP 6  
DB 1 GRGDTTP 6  
RESULT 6  
AAY31127  
ID AAY31127 standard; peptide: 6 AA.  
XX AC AAY31127:  
XX  
DT 21-OCT-1999 (first entry)  
DE Non-crosslinked protein particle peptide 176.  
XX  
KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
KW albumin; haemoglobin; nanometer; micrometer; clearance.  
XX  
OS Synthetic.  
XX

```

PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PF 12-NOV-1996; 9405-0747137.
XX
PR 14-MAR-1994; 9405-0212546.
PR 15-JAN-1991; 9105-0641720.
PR 13-OCT-1992; 9205-0953560.
PR 01-JUN-1993; 9205-0953560.
PR 12-NOV-1996; 9605-0747137.
XX
PA (HEMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI: 1999-508153/42.
XX
PT Non-crosslinked protein particles for therapeutic and diagnostic use
XX
PS Example 22; Column 123-124; 65pp; English.
XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles of non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30952-Y31135 represent peptides used in the method of the invention.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRGTRP 6
DB 1 GRGTRP 6
RESULT 7
AAY31025
XX AAY31025 standard; peptide: 6 AA.
XX
AC AAY31025;
XX
DT 21-OCT-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 74.
XX
KW Non-crosslinked protein particles; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PF 12-NOV-1996; 9605-0747137.
XX
PR 14-MAR-1994; 9405-0212546.
PR 15-JAN-1991; 9105-0641720.
PR 13-OCT-1992; 9205-0953560.
PR 01-JUN-1993; 9305-0065831.

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PR 12-NOV 1996; 9605-0747137.
XX
PA (HEMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI: 1999-508153/42.
XX
PT Non-crosslinked protein particles for therapeutic and diagnostic use
XX
PS Example 22; Column 81-82; 65pp; English.
XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles of non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30952-Y31135 represent peptides used in the method of the invention.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRGTRP 6
DB 1 GRGTRP 6
RESULT 8
AAY84459
XX AAY84459 standard; Peptide: 6 AA.
XX
AC AAY84459;
XX
DT 25-MAR-1999 (first entry)
XX
DE RGD peptide that stimulates cell invasion by S. pyogenes 90-226.
XX
KW Streptococcus pyogenes 90-226; pathogen; inhibition;
KW cell adhesion; cell invasion; treatment; bacterial; infection;
KW fungal infection.
XX
OS Synthetic.
XX
PN WO9856428-A2.
XX
DT 17-DEC-1996.
XX
PR 10-JUN-1998; 98WO-US12019.
XX
PR 10-JUN-1997; 97US-0049124.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Cleary PP, Cue DR;
XX
DR WPI: 1999-080856/07.
XX
PT Method for treating mammal infected by pathogenic microorganism -
PT comprises administering to mammal composition comprising inhibitory
PT compound which inhibits adherence to or invasion of a cell by
PT microorganism
XX

```

PS Example 2; Page 43; 58pp; English.

XX The present sequence represents a RGD peptide that is able to  
CC stimulate cell invasion by Streptococcus pyogenes 93-225. The  
CC peptides were used in the course of the invention. The  
CC specification describes the treatment of a mammal infected  
CC by a pathogenic microorganism which comprises administering an  
CC inhibitory compound to inhibit adherence to or invasion of cells  
CC by the pathogen. The method is used in the treatment of bacterial  
CC or fungal infection.

XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 35; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGTP 6  
Db 1 GRGTP 6

RESULT 9  
AA528163  
ID AAB28163 standard; peptide: 6 AA.

XX  
AC AA528163;  
DT 09-FEB-2001 (first entry)

XX Peptide #3 used to assay vitronectin receptor binding inhibition.

DE Antiviral; antiinflammatory; cytostatic; vasotropic; antitumour;  
XX antiarthritic; ophthalmological; osteopathic;  
KW amido-carboxylic acid derivative; cancer; angiogenesis;  
KW neovascularisation; macular degeneration; glaucoma; blindness;  
KW rheumatoid arthritis; restenosis; viral infection; bone resorption;  
KW osteoporosis; osteopenia; periodontal disease; hyperparathyroidism;  
KW Paget's disease; integrin vitronectin receptor; alpha\_vbeta\_3; melanoma.

XX Unidentified.  
XX  
XX W0200061545-A1.

XX 10-OCT-2000.  
XX  
XX 13-APR-2000; 2000W0-US10027.

XX 14-APR-1999; 99US-0291470.  
XX  
XX (AMHP ) AMERICAN HOME PROD CORP.

XX  
XX Gopalasamy A, Yang HY;  
XX  
XX WPI; 2000-687029/67.

XX  
XX  
XX New amido-carboxylic acid derivatives are integrin inhibitors used for  
PT treating e.g. cancer, restenosis, osteoporosis, viral infection and  
PT bone disease.

XX Disclosure; Page 17; 67pp; English.

XX The present invention relates to amido-carboxylic acid derivatives. The  
CC amido-carboxylic acid derivatives may be used for treating cancer,  
CC angiogenesis, neovascularisation, macular degeneration, glaucoma,  
CC blindness, rheumatoid arthritis, restenosis, smooth cell proliferation  
CC and migration, vascular endothelial cell proliferation and migration,  
CC viral infection (characterised by bone resorption of mineralised  
CC tissues), osteoporosis, hypercalcaemia of malignancy, osteopenia due to  
CC bone metastasis, periodontal disease, hyperparathyroidism, periarticular  
CC erosions in rheumatoid arthritis, Paget's disease, immobilisation-induced  
CC osteopenia or glucocorticoid treatment, or diseases characterised by some  
CC resorption of mineralised tissues. The present sequence is a peptide.

CC which was used as a reference compound in an assay for the ability of the  
CC amido-carboxylic acid derivatives of the present invention to inhibit  
CC integrin vitronectin receptor (alpha\_vbeta\_3) binding. Integrin  
CC alpha\_vbeta\_3 has been shown to mediate the invasion of cancerous  
CC melanoma cells into healthy tissue and to protect these cells against  
CC apoptosis. In addition, vitronectin receptor antagonists have been shown  
CC to inhibit the growth of various solid tumours of human origin.

XX Sequence 6 AA;

XX  
SQ  
Query Match 100.0%; Score 35; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGTP 6  
Db 1 GRGTP 6

RESULT 10  
AA586475  
ID AAY86475 standard; peptide: 6 AA.

XX  
AC AAY86475;  
DT 06-JUN-2000 (first entry)

XX Cell adhesion peptide #10.

XX Bone regenerative; osteopathic; osseous tissue; reconstitution;  
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;  
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.

XX Synthetic.

XX W02000604941-A1.

XX 03-FEB-2000.

XX 22-JUL-1999; 99W0-US16800.

XX 24-JUL-1996; 98US-012348.

XX (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.

XX Sudny JA;

XX WPI; 2000-195084/17.

XX System for reconstructing osseous tissue, useful e.g. for treating  
PT fractures, comprises scaffold containing promoter of bone formation and  
PT inhibitor of bone resorption.

XX Claim 14; Page 31; 44pp; English.

XX The invention relates to a novel system for reconstruction of osseous  
CC tissue comprising a scaffold carrying a compound (I) that promotes  
CC bone formation and a component that decreases bone resorption (II).  
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and  
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular  
CC matrix. (I) is preferably selected from: selectin or selectin binding  
CC fragments, proteins and peptides that facilitate cell adhesion,  
CC plasminogen activator inhibitors, protease inhibitors and  
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed  
CC examples of cell adhesion peptides used in the system of the invention.  
CC The system is used to replace, remodel or correct bone defects, e.g.  
CC fractures, fissures or bone mass loss. Incorporation of (I) into the  
CC scaffold results in rapid seeding by osteoblasts and the development of  
CC an organic matrix, i.e. the preformed scaffold replaces the  
CC rate-determining step of extracellular matrix formation. The scaffold can  
CC be designed to have a predetermined resorption/degradation rate, and may  
CC include regulatory compounds for specific cell types.

SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 DB 1 GRGDTF 6

RESULT 11  
 AAB91972  
 ID AAB91972 standard; peptide: 6 AA.  
 XX  
 AC AAB91972;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:114P.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimide group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.  
 XX  
 PS 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US13576.  
 XX  
 PR 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX  
 PA (CONJ-) CONJUCHEM INC.  
 XX  
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX  
 WPI: 2001-1:2059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT  
 XX  
 PS Disclosure; Page 571; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimide and maleimide groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as binding to large molecules increases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 DB 1 GRGDTF 6

RESULT 12  
 ABB40076  
 ID ABB40076 standard; peptide: 6 AA.  
 XX  
 AC ABB40076;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Integrin modulator peptide #3.  
 XX  
 KW Neurodegenerative disease; amyloid; neuroprotective; anti Alzheimer's;  
 KW Alzheimer's disease; integrin; therapeutic agent.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2002226107-A2.  
 XX  
 PF 04-APR-2002.  
 XX  
 PS 25-SEP-2001; 2001WO-US29788.  
 XX  
 PR 25-SEP-2000; 2000US-235374P.  
 XX  
 PA (KESC) UNIV CALIFORNIA.  
 XX  
 PI Lynch G, Xiaoning B, Gall CW;  
 XX  
 WPI: 2002-416420/44.  
 XX  
 PT Experimental models for studying neurodegenerative diseases associated with amyloid accumulation, useful for studying e.g. Alzheimer's disease and for identifying potential therapeutic agents -  
 XX  
 PS Claim 15; Page 63; 80pp; English.  
 XX  
 CC The invention relates to experimental models for studying neurodegenerative diseases associated with amyloid accumulation. The activity of peptides of the invention may be described as neuroprotective and anti-Alzheimer's. They act by inhibiting amyloid accumulation. The experimental model may be used to study neurodegenerative diseases associated with amyloid accumulations, e.g. Alzheimer's disease and to identify potential therapeutic agents for treating those diseases. The current sequence represents an integrin modulator peptide of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 DB 1 GRGDTF 6

RESULT 13  
 AAR34612  
 ID AAR34612 standard; protein: 6 AA.  
 XX  
 AC AAR34612;  
 XX  
 DT 25-MAR-2003 (updated)  
 XX  
 PS 05-SEP-1990 (first entry)  
 XX  
 DE Antiviral agent.  
 XX

KW Antiviral; M2; poliovirus; folio; hepatitis.  
 OS Synthetic.  
 XX JP02078631-A.  
 PN  
 XX 19-MAR-1990.  
 PD  
 XX 14-SEP-1988; 88JP-0228943.  
 PF  
 XX 14-SEP-1988; 88JP-0228843.  
 PR  
 XX (NIHA ) NIPPON MENINS CO.  
 PA  
 XX WPI; 1990-129060/17.  
 DR  
 XX Antiviral agent contg. tripeptide (unit) -  
 PT of basic aminoacid, then alanine, glycine or sarcosine, and  
 PT acidic aminoacid, effective against virus with protein-terminated RNA  
 PT or RNA.  
 XX Disclosure; Page 2; 4pp; Japanese.  
 PS  
 XX Peptide is effective against inhibiting propagation of DNA or RNA  
 CC bonded, protein containing viruses ex. Poliovirus, Hepatitis virus.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 88.6%; Score 31; DR 11; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 OY 1 GRGDTP 6  
 DB 1 GRGDSP 6  
 RESULT 14  
 ID AAR06455 standard; peptide; 6 AA.  
 XX AAR06455;  
 AC  
 XX 25-MAR-2004 (updated)  
 DT 04-JAN-1991 (first entry)  
 DI  
 XX Fibrinectin derived RGD-contg. peptide.  
 DE  
 XX Tenascin; receptor; tumour.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9008781-A.  
 PN  
 XX 09-AUG-1990.  
 PD  
 XX 23-JAN-1990; 90WO-US00408.  
 PE  
 XX 24-JAN-1989; 89US-0302755.  
 PR  
 XX (LJOL-) LA JOLLA CANCER RES FOUND.  
 PA  
 XX Ruoslahti Et., Bourdon MA;  
 PI  
 XX WPI; 1990-260895/34.  
 DR  
 XX Tenascin-induced cell attachment - interacts with tenascin in  
 PT arginine-glycine-asparagine dependent manner.  
 XX  
 PS Example II; Page 9; 22pp; English.  
 CC The peptide was used in cell attachment assays to show inhibition.

CC of attachment to tenascin by Arg-Gly Asp contg. peptides. It  
 CC completely inhibited attachment at a concn. of 300-900 nM. 30- and  
 CC 50-fold lower than needed for comparable inhibition of cell  
 CC attachment to vitronectin and fibronectin resp.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 88.6%; Score 31; DR 11; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 OY 1 GRGDTP 6  
 DB 1 GRGDSP 6  
 RESULT 15  
 ID AAR29063 standard; peptide; 6 AA.  
 XX AAR29063;  
 AC  
 XX 20-MAY-1998 (first entry)  
 DT  
 XX Peptide contg. RGD motif as a side chain to a water sol. polymer.  
 DE  
 XX Adhesive peptide; cell adhesion; inhibitor; platelet aggregation.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 PH Modified\_site 1  
 PT Modified\_site 6 /note= "alkylated/arylated"  
 PE Modified\_site 6 /note= "alkylated/arylated"  
 PF JP04221396-A.  
 XX 11-AUG-1992.  
 BU  
 XX 20-DEC-1990; 90JP-0404347.  
 PF  
 XX 20-DEC-1990; 90JP-0404347.  
 PE  
 XX (FUJF ) FUJII PHOTO FILM CO LTD.  
 PA  
 XX WPI; 1992-313680/38.  
 CR  
 XX Water-soluble vinyl polymer deriv. for animal cell adhesion  
 PI inhibitor or platelet aggregation inhibitor  
 PS Example; Page 12; 14pp; Japanese.  
 XX The peptide sequence contains the Arg-Gly-Asp motif of cell  
 CC adhering proteins. It comprises the essential unit of a  
 CC water-sol. vinyl polymer with a pref. mol. wt. of 3000-100,000 D.  
 CC The polymer shows various biological activities, e.g. immunological  
 CC coordination, wound healing action and platelet aggregation inhibiting  
 CC action etc. See also AAR29062-8.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 88.6%; Score 31; DR 13; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 OY 1 GRGDTP 6  
 DB 1 GRGDSP 6

Search completed: September 16, 2003. 18:19:41



GenCore version 5.1.6  
 Copyright (c) 1993 - 2003 CompuGen Ltd.  
 OM protein - protein search, using sw model  
 Run on: September 16, 2003, 15:19:48 : Search time 25 Seconds  
 (without alignments)  
 35,734 Million cell updates/sec

Title: US-09-780-612A 1  
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Scoring table: BLASTM62  
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Searched: 556269 seqs, 14889469 residues

Total number of hits satisfying chosen parameters: 15287

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 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	12	US-10-420-029-1
2	35	100.0	6	14	US-10-007-270-35
3	35	100.0	6	15	US-10-263-455-1
4	31	88.6	6	9	US-09-847-969A-26
5	31	88.6	6	9	US-09-837-969A-46
6	31	88.6	6	9	US-09-888-260-15
7	31	88.6	6	9	US-09-961-834-1
8	31	88.6	6	10	US-09-364-597A-21
9	31	88.6	6	10	US-09-177-843-1
10	31	88.6	6	10	US-09-841-323A-28
11	31	88.6	6	10	US-09-841-323A-46
12	31	88.6	6	10	US-09-871-974-3
13	31	88.6	6	10	US-09-972-772-31
14	31	88.6	6	12	US-10-262-435-5
15	31	88.6	6	12	US-10-425-021-9

16	31	88.6	6	14	US-10-081-945-41
17	31	88.6	6	14	US-10-007-270-32
18	31	88.6	6	14	US-10-007-270-35
19	31	88.6	6	14	US-10-114-176-2
20	31	88.6	6	15	US-10-046-801-5
21	31	88.6	6	15	US-10-237-850-83
22	31	88.6	6	15	US-10-136-935-31
23	29	82.9	6	10	US-09-963-206B-10
24	29	82.9	6	10	US-09-916-940-3
25	29	82.9	6	10	US-09-792-630-54
26	29	82.9	6	10	US-09-965-976A-10
27	29	82.9	6	12	US-10-086-550-5
28	29	82.9	6	14	US-10-050-376-54
29	29	82.9	6	14	US-10-061-395-2
30	29	82.9	6	15	US-10-053-355A-7
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32	27	77.1	6	10	US-09-364-597A-23
33	27	77.1	6	10	US-09-177-843-2
34	27	77.1	6	12	US-10-375-942-17
35	27	77.1	6	12	US-10-420-029-2
36	27	77.1	6	15	US-10-237-850-84
37	27	77.1	6	15	US-13-264-374-17
38	25	71.4	5	11	US-09-911-569-14
39	25	71.4	5	12	US-10-200-879-11
40	25	71.4	5	12	US-10-325-021-23
41	25	71.4	6	9	US-09-892-071-5
42	25	71.4	6	11	US-09-911-569-14
43	25	71.4	6	12	US-10-210-879-14
44	25	71.4	6	14	US-10-007-270-34
45	24	68.6	5	9	US-09-096-749A-72

## ALIGNMENTS

RESULT 1  
 US-10-420-029-1  
 : Sequence 1, Application US10420029  
 : Publication No. US20030157712A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Daniel, Thomas O.  
 : APPLICATOR: Steis, Elke  
 : TITLE OF INVENTION: Methods for Determining Cell Responses  
 : TITLE OF INVENTION: Through FprB Receptors  
 : FILE REFERENCE: 22000.508502  
 : CURRENT APPLICATION NUMBER: US10/420,029  
 : CURRENT FILING DATE: 2003-04-17  
 : PRIOR APPLICATION NUMBER: 09/485,653  
 : PRIOR FILING DATE: 2000-02-14  
 : PRIOR APPLICATION NUMBER: PCT/US98/17157  
 : PRIOR FILING DATE: 1998-08-19  
 : PRIOR APPLICATION NUMBER: 60/056,164  
 : PRIOR FILING DATE: 1997-08-19  
 : NUMBER OF SEQ ID NOS: 3  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 1  
 : LENGTH: 6  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence; No. US20030157712A1e -  
 : OTHER INFORMATION: synthetic construct  
 US-10-420-029-1

Query Match 100.0%; Score 35; DB 12; Length 6;

Best Local Similarity 100.0%; Pred. No. 56+05; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;

QY 1 GRGDTF 6

DB 1 GRGDTF 6



RESULT 2  
 US-10-007-270-33  
 : Sequence 33, Application US/16007270  
 : Publication No. US20020160954A;  
 : GENERAL INFORMATION:  
 : APPLICANT: Hagaman, Gregory S.  
 : APPLICANT: Kuhn, Markus H.  
 : TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 : FILE REFERENCE: 020618-00312005  
 : CURRENT APPLICATION NUMBER: US/10/007,270  
 : CURRENT FILING DATE: 2001-11-30  
 : PRIOR APPLICATION NUMBER: US 09/430,195  
 : PRIOR FILING DATE: 1999-10-29  
 : PRIOR APPLICATION NUMBER: US 09/187,472  
 : PRIOR FILING DATE: 1998-10-29  
 : NUMBER OF SEQ ID NOS: 37  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 33  
 : LENGTH: 6  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence:  
 : OTHER INFORMATION: RGD-containing peptide  
 : US-10-007-270-33

Query Match 100.0% Score 35; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 56-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTG 6  
 DB 1 GRGDTG 6

RESULT 3  
 US-10-263-456-1  
 : Sequence 1, Application US/10263456  
 : Publication No. US2003007646A1  
 : GENERAL INFORMATION:  
 : APPLICANT: GREG BIESECKER  
 : SCMEDHA D. JAYASENA  
 : LARRY GOLD  
 : DREW SMITH  
 : GARY P. KIPSCHNEIDER  
 : TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
 : EXPONENTIAL ENRICHMENT: BLENDED  
 : SELEX  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Swanson & Bratsberg, L.L.C.  
 : STREET: 2745 Shea Center Drive, Suite 310  
 : CITY: Highlands Ranch  
 : STATE: Colorado  
 : COUNTRY: USA  
 : ZIP: 80129  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: MS-DOS  
 : SOFTWARE: WordPerfect 8.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/10/263,456  
 : FILING DATE: 02-Oct-2002  
 : CLASSIFICATION: <Unknown>  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/605,477  
 : FILING DATE: 29-Jun-2000  
 : APPLICATION NUMBER: 08/956,699  
 : FILING DATE: OCTOBER 23, 1997  
 : APPLICATION NUMBER: 08/234,997  
 : FILING DATE: APRIL 28, 1994

APPLICATION NUMBER: 07/714,131  
 FILING DATE: JUNE 10, 1991  
 APPLICATION NUMBER: 07/536,425  
 FILING DATE: JUNE 11, 1990  
 APPLICATION NUMBER: 08/177,991  
 FILING DATE: SEPTEMBER 8, 1993  
 APPLICATION NUMBER: 08/123,935  
 FILING DATE: SEPTEMBER 17, 1993  
 APPLICATION NUMBER: 08/199,507  
 FILING DATE: FEBRUARY 22, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 REFERENCE/DOCKET NUMBER: NEX15/L-CON  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 793-3339  
 TELEFAX: (303) 793-3453  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 6 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US 10-263-456-1

Query Match 100.0% Score 35; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 56-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTG 6  
 DB 1 GRGDTG 6

RESULT 4  
 US-09-837-969A-28  
 : Sequence 28, Application US/09837969A  
 : Patent No. US20020038150A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Univ. Dan  
 : TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
 : FILE REFERENCE: BERL-020/0305  
 : CURRENT APPLICATION NUMBER: US/09/837,969A  
 : CURRENT FILING DATE: 2001-06-19  
 : PRIOR APPLICATION NUMBER: US 09/258,723  
 : PRIOR FILING DATE: 1999-02-26  
 : PRIOR APPLICATION NUMBER: US 60/087155  
 : PRIOR FILING DATE: 1998-05-29  
 : PRIOR APPLICATION NUMBER: US 60/076297  
 : PRIOR FILING DATE: 1998-02-27  
 : NUMBER OF SEQ ID NOS: 65  
 : SOFTWARE: PatentIn version 3.0  
 : SEQ ID NO 28  
 : LENGTH: 6  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : NAME/KEY: PEPTIDE  
 : LOCATION: (1)..(6)  
 : OTHER INFORMATION: Synthetic  
 : US-09-837-969A-28

Query Match 88.6% Score 31; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 56-05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTG 6  
 DB 1 GRGDTG 6

RESULT 5

US-09-837-969A-46  
; Sequence 46, Application US/09837969A  
; Patent No. US2002038130A1  
; GENERAL INFORMATION:  
; APPLICANT: Urry, Dan  
; TITLE OF INVENTION: Infectable Implants For Tissue Augmentation and Res.Grafting  
; FILE REFERENCE: BERL-020/0305  
; CURRENT APPLICATION NUMBER: US/09/837,969A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/258,723  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: US 60/087155  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: US 60/076297  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 46  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(6)  
; OTHER INFORMATION: Synthetic  
US-09-837-969A-46

Query Match 88.6%; Score 31; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6  
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DB 1 GRGDSP 6

RESULT 6  
US-09-888-260-15  
; Sequence 15, Application US/09888260  
; Patent No. US2002006304A1  
; GENERAL INFORMATION:  
; APPLICANT: Bioclastics Research, Ltd.  
; APPLICANT: Urry, Dan  
; TITLE OF INVENTION: Hioelastomer Nanomachines and Biosensors  
; FILE REFERENCE: BERL-030/0105  
; CURRENT APPLICATION NUMBER: US/09/888,260  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/213,364  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(6)  
; OTHER INFORMATION: Synthetic  
US-09-888-260-15

Query Match 88.6%; Score 31; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6  
|||||  
DB 1 GRGDSP 6

RESULT 7  
US-09-961-834-1  
; Sequence 1, Application US/09961834

Patent No. US20020081726A1  
; GENERAL INFORMATION:  
; APPLICANT: Russell et al.  
; TITLE OF INVENTION: MICROFABRICATION OF MEMBRANES FOR THE GROWTH OF CELLS  
; FILE REFERENCE: 27611/37761  
; CURRENT APPLICATION NUMBER: US/09/961,814  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/235,094  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Fibronectin: ligand receptor  
US-09-961-834-1

Query Match 88.6%; Score 31; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6  
|||||  
DB 1 GRGDSP 6

RESULT 8  
US-09-364-597A-21  
; Sequence 21, Application US/09364597A  
; Patent No. US20020133130A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Koivunen, Erkki  
; TITLE OF INVENTION: NO. US20020133130A1: Interic-binding Reptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentia Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/364,597A  
; FILING DATE: 30-JUL-1999  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US 06/158,001  
; FILING DATE: 24-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/286,861  
; FILING DATE: 04-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 3419  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (858) 535-9001  
; TELEFAX: (858) 535-8949  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-364-597A-21

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDP 6  
1 1111  
DB 1 GRGDP 6

## RESULT 9

US-09-177-843-1  
Sequence 1, Application US/0917784;  
Patent No. US20020114804A1  
GENERAL INFORMATION:  
APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE  
APPLICANT: CITY OF NEW YORK  
TITLE OF INVENTION: A METHOD OF PREVENTING AND TREATING  
TITLE OF INVENTION: BACTERIAL INFECTION OF SUTURES AND  
TITLE OF INVENTION: PROSTHETIC DEVICES, AND PROMOTING  
TITLE OF INVENTION: INGRESS OF LEUKOCYTES INTO TUMOR  
TITLE OF INVENTION: FOCI  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1165 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent release #1.0, Version #1.3C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,843  
FILING DATE: April 22, 1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 48940-A-PCT/JFW/JKM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-09-177-843-1

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. Seqs: 1;  
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDP 6  
1 1111  
DB 1 GRGDP 6

## RESULT 10

US-09-841-321A-28  
Sequence 28, Application US/09841321A  
Patent No. US20020116069A1  
GENERAL INFORMATION:  
APPLICANT: Urry, Dan  
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
FILE OF INVENTION: BERL-020/0405  
CURRENT APPLICATION NUMBER: US/09/841,321A  
CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: US 09/258,723  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: US 60/087155  
PRIOR FILING DATE: 1998-05-23  
PRIOR APPLICATION NUMBER: US 60/076297  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)...(6)  
OTHER INFORMATION: Synthetic  
US-09-841-321A-28

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. Seqs: 1;  
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDP 6  
1 1111  
DB 1 GRGDP 6

## RESULT 11

US-09-841-321A-46  
Sequence 46, Application US/09841321A  
Patent No. US20020116069A1  
GENERAL INFORMATION:  
APPLICANT: Urry, Dan  
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
FILE OF INVENTION: BERL-020/0405  
CURRENT APPLICATION NUMBER: US/09/841,321A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 09/258,723  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: US 60/087155  
PRIOR FILING DATE: 1998-05-23  
PRIOR APPLICATION NUMBER: US 60/076297  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 46  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)...(6)  
OTHER INFORMATION: Synthetic  
US-09-841-321A-46

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. Seqs: 1;  
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDP 6  
1 1111  
DB 1 GRGDP 6

## RESULT 12

US-09-871-974-3  
Sequence 3, Application US/09871974  
Patent No. US20020147136A1  
GENERAL INFORMATION:  
APPLICANT: VON WRONSKI, MATHEW A.  
APPLICANT: MARINELLI, EDMUND R.  
APPLICANT: NURN, ADRIAN D.  
APPLICANT: PILLAI, RADHAKRISHNA

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1  APPLICANT: KAMALINGAM, KONDAREDDYAP
2  APPLICANT: TREHLE, MICHAEL F.
3  APPLICANT: LINDER, KAREN
4  APPLICANT: NANJAPPAN, PALANIAPPA
5  APPLICANT: RAJU, NATARAJAN
6  TITLE OF INVENTION: COMPOUNDS FOR TARGETING ENDOTHelial CELLS, COMPOSITIONS
7  FILE REFERENCE: 2238-7
8  CURRENT APPLICATION NUMBER: US/09/871,974
9  CURRENT FILING DATE: 2001-06-04
10 PRIOR APPLICATION NUMBER: 09/585,164
11 PRIOR FILING DATE: 2000-06-02
12 NUMBER OF SEQ ID NOS: 13
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 3
15 LENGTH: 6
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
20 US-09-871-974-3
21
22 Query Match      88.6%  Score 31:  DB 10:  Length 6:
23 Best Local Similarity 83.3%  Pred. No. 5e+05:
24 Matches 5:  Conservative 1:  Mismatches 0:  Indels 0:  Gaps 0:
25
26 QY 1 GRGDTP 6
27      III:I
28 Db 1 GRGDSP 6
29
30 RESULT 13
31 US-09-972-772-31
32 Sequence 31: Application US/09972772
33 Publication No. US20020193298A1
34 GENERAL INFORMATION:
35 APPLICANT: Olson, Gary L.
36 APPLICANT: Seif, Christopher
37 APPLICANT: Lee, Lily
38 APPLICANT: Cook, Charles M.
39 TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
40 TREATMENT OF ANGIOGENESIS
41 FILE REFERENCE: PPT-106CP
42 CURRENT APPLICATION NUMBER: US/09/972-772
43 CURRENT FILING DATE: 2001-10-05
44 PRIOR APPLICATION NUMBER: US 09/704,251
45 PRIOR FILING DATE: 2000-11-01
46 NUMBER OF SEQ ID NOS: 35
47 SOFTWARE: PatentIn Ver. 2.0
48 SEQ ID NO 31
49 LENGTH: 6
50 TYPE: PRT
51 ORGANISM: Artificial Sequence
52 FEATURE:
53 OTHER INFORMATION: Description of Artificial Sequence: Motifs
54 US-09-972-772-31
55
56 Query Match      88.6%  Score 31:  DB 10:  Length 6:
57 Best Local Similarity 83.3%  Pred. No. 5e+05:
58 Matches 5:  Conservative 1:  Mismatches 0:  Indels 0:  Gaps 0:
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60 QY 1 GRGDTP 6
61      III:I
62 Db 1 GRGDSP 6
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64 RESULT 14
65 US-10-262-435-5
66 Sequence 5: Application US/0262435
67 Publication No. US20030166832A1
68 GENERAL INFORMATION:
69 APPLICANT: Goldstein, Gideon
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GS-10-325-021-9

Query Match 88.6%; Score 31; DS 12; Length 6;  
Best Local Similarity 81.3%; Pred. NO. Se-05;  
Matches 5; Conservative 1; Mismatches 2; Gaps 0;

QY 1 GRGDP 6  
DB 1 GRGDP 6

Search completed: September 16, 2003, 18:21:52  
Job time : 25 sec's

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 14:18:28 ; Search time 14 Seconds  
(without alignments)  
41,215 Million cell updates/sec

Title: US-09-780-612a-1  
Perfect score: 35  
Sequence: 1 GRGCTP 6

Scoring table: BLAST/MSM2  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96:69682 res.dues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR75:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being listed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	51.4	6	2 PT0280	IG heavy chain CRD3 region (clone 4-91B) - human (fragment)
2	17	48.6	5	2 PT0608	T-cell receptor be
3	17	48.6	5	2 PT0690	T-cell receptor be
4	17	48.6	6	2 151434	IG heavy chain CRD3 region (clone 4-91B) - human (fragment)
5	17	48.6	6	2 PT0630	T-cell receptor be
6	13	37.1	6	2 PT0514	T-cell receptor be
7	12	34.3	4	2 S17255	ribosomal protein
8	12	34.3	4	2 PT0711	T-cell receptor be
9	12	34.3	5	2 P20689	photosystem I subunit
10	12	34.3	5	2 PT0513	T-cell receptor be
11	12	34.3	5	2 PT0538	T-cell receptor be
12	12	34.3	5	2 PT0703	T-cell receptor be
13	12	34.3	5	2 PT0573	T-cell receptor be
14	12	34.3	5	2 PT0679	T-cell receptor be
15	12	34.3	6	2 S76764	ribosomal protein
16	12	34.3	6	2 PT0629	T-cell receptor be
17	12	34.3	6	2 PT0511	T-cell receptor be
18	12	34.3	6	2 PT0604	T-cell receptor be
19	12	34.3	6	2 PT0687	T-cell receptor be
20	12	34.3	6	2 PT0652	T-cell receptor be
21	12	34.3	6	2 PT0587	T-cell receptor be
22	12	34.3	6	2 PT0568	T-cell receptor be
23	12	34.3	6	2 PT0709	T-cell receptor be
24	11	31.4	4	1 ECXAA	antho-ramide neur
25	11	31.4	4	2 A25844	antho-ramide neur
26	11	31.4	4	2 S47552	ubiquitin - rat
27	11	31.4	5	2 C23751	spinal cord peptid
28	11	31.4	5	2 140702	primase - Citrobac
29	11	31.4	5	2 B31816	20K protein - Rick

30	11	31.4	5	2 S53595	hypothetical prote
31	11	31.4	5	2 D44823	synaposomal-assoc
32	11	31.4	5	2 C53284	T-cell receptor be
33	11	31.4	5	2 PT0525	T-cell receptor be
34	11	31.4	5	2 PT0553	T-cell receptor be
35	11	31.4	5	2 PT0561	T-cell receptor be
36	11	31.4	5	2 PT0635	T-cell receptor be
37	11	31.4	5	2 PT0700	T-cell receptor be
38	11	31.4	6	2 A63494	anticoagulant gly
39	11	31.4	6	2 A45474	epsilon IL1b -
40	11	31.4	6	2 PT0605	T-cell receptor be
41	11	31.4	6	2 PT0619	T-cell receptor be
42	11	31.4	6	2 PT0668	T-cell receptor be
43	11	31.4	6	2 PT0723	T-cell receptor be
44	11	31.4	6	2 A45946	T-cell receptor ga
45	10	28.6	4	2 A53284	T-cell receptor be

## ALIGNMENTS

RESULT 1  
PT0280  
IG heavy chain CRD3 region (clone 4-91B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #ext\_change 16-Aug-1996  
C:Accession: PT0280  
R:Manada, K.; Wasserman, R.; Reichard, B.A.; Shaw, S.; Caton, A.L.; Rivera, G.  
C:Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity at  
A:Reference number: PT0222; M010:9108337; PMID:1899102  
A:Accession: PT0280  
A:Molecule type: DNA  
A:Residues: 116 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 51.4% Score 18; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGCTP 6  
DB 1 GSGSAP 6

RESULT 2  
PT0608  
T-cell receptor beta chain V-D-J region (120-208) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #ext\_change 30-May-1997  
C:Accession: PT0608  
R:Feeney, A.J.  
C:Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of total T cell receptor beta chains have few N regions  
A:Reference number: PT0509; M010:91277601; PMID:1711558  
A:Accession: PT0608  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <PFE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 48.6% Score 17; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 3 GRG 5

RESULT 3

PT0690  
T-cell receptor beta chain V-D-J region (240-180) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0690  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0590  
A>Status: translation not shown  
A:Molecule type: cDNA  
A:Residues: 1-5 <FE>  
A:Experimental source: day 16 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 48.6%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDT 5  
DB 3 GDT 5

RESULT 4  
151434  
H4 histone - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: 151434  
R:Woodland, H.R.; Warminston, J.R.; Ballantyne, J.F.M.; Turner, P.C.  
Nucleic Acids Res. 12, 4939-4959, 1984  
A:Title: Are there major developmentally regulated H4 gene classes in Xenopus?  
A:Reference number: 151391; MUID:84247348; PMID:633669;  
A:Accession: 75434  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <WO>  
A:Cross-references: GB:K02304; MLD:q214227; PIR:AAA49738.1; PDB:q595517

Query Match 48.6%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 3 GRG 5

RESULT 5  
PT0630  
T-cell receptor beta chain V-D-J region (111-10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0630  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0630  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 48.6%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDT 5  
DB 3 GDT 5

DB 3 GDT 5

RESULT 6  
PT0514  
T-cell receptor beta chain V-D-J region (100-40) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0514  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0514  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 37.1%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e-05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 4 GRG 6

RESULT 7  
S17255  
ribosomal protein YRL1, mitochondrial, questionable yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
A:Variety: strain 07173  
C:Date: 21-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 05-May-1997  
C:Accession: S17255  
R:Gromann, L.; Graack, H.R.; Kraft, V.; Chelli, T.; Goldschmidt-Helms, S.; Kitakawa, F.B.S. Lett. 284, 51-56, 1993  
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit fr  
A:Reference number: S17255; MUID:91265106; PMID:2050626  
A:Accession: S17255  
A:Molecule type: protein  
A:Residues: 1-4 <GR>  
C:Comment: A coding region for this protein could not be identified in the genome of  
C:Genetics:  
A:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 34.3%; Score 12; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TP 6  
DB 3 TP 4

RESULT 8  
PT0711  
T-cell receptor beta chain V-D-J region (120-23) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0607; PT0674; PT0678; PT0670; PT0710  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0607  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FE>  
A:Experimental source: newborn thymus, strain BALB/c, 120-2J  
A:Accession: PT0674

```

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A:Accession: P0678
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A:Accession: P0576
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FE4>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A:Accession: P0711
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FE5>
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C:Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 GD 4
DB      3 GD 4

RESULT 9
PQ0589
Photosystem I D1, 4K H1 chain, common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #ext_change 17-Mar-1995
C:Accession: PQ0689
R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A:Title: Molecular heterogeneity of photosystem I, psal, psae, psaf, psah and psal are a
A:Reference number: PQ0689
A:Accession: PQ0689
A:Molecule type: protein
A:Residues: 1-5 <OH0>
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match      34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 GD 4
DB      3 GD 4

RESULT 10
PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #ext_change 30-May-1997
C:Accession: PT0513; PT0606
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0513
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE>
A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A:Accession: PT0606
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>

A:Experimental source: newborn thymus, strain BALB/c, clone 126-1F
C:Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 GD 4
DB      3 GD 4

RESULT 11
PT0539
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #ext_change 30-May-1997
C:Accession: PT0538; PT0539; PT0603
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0538
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A:Accession: PT0539
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE3>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
A:Accession: PT0603
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C:Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 GD 4
DB      3 GD 4

RESULT 12
PT0703
T-cell receptor beta chain V-D-J region (145-1F) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #ext_change 30-May-1997
C:Accession: PT0703
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0703
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      3 GD 4
DB      3 GD 4

```



## RESULT 13

PT0573  
 T-cell receptor beta chain V-D-J region (141-160) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0573  
 R:Feeney, A.J.,  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; M015:9127760-; PMID:1711556  
 A:Accession: PT0573  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <PEP>  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
 II  
 DB 3 GD 4

## RESULT 14

PT0679  
 T-cell receptor beta chain V-D-J region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30 May 1997  
 C:Accession: PT0679; PT0708  
 R:Feeney, A.J.,  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; M015:9127760-; PMID:1711556  
 A:Accession: PT0679  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PEP>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-21  
 A:Accession: PT0708  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PE2>  
 A:Experimental source: newborn thymus, strain BALB/c, 151-28  
 C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
 II  
 DB 3 GD 4

## RESULT 15

S78764  
 ribosomal protein Mkp-S23, mitochondria; bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: S78764  
 R:Graack, H.R.,  
 submitted to the Protein Sequence Database, July 1999  
 A:Reference number: S78760  
 A:Accession: S78764  
 A:Molecule type: protein  
 A:Residues: 1-6 <GRA>  
 C:Keywords: mitochondrion  
 F:1-6/Product: ribosomal protein Mkp-S23 (fragment) #status experimental - EAT

Query Match 34.3%; Score 12; DB 2; Length 5;  
 Best Local Similarity 95.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 4 GD 6  
 II  
 DB 4 DKP 6

Search completed: September 16, 2003, 18:20:58  
 Job time: 14 secs

Result No.	Score	Query Match	Length	EB	ID	Accession
1	25	42.9	4	1	OXPL_OCTM	P58648 octopus msh
2	33	37.1	5	1	OXB4_OCTM	P38925 chlamydia
3	12	34.3	4	1	RW01_YEAST	P35515 saccharomyce
4	12	34.3	5	1	TR01_YEBCU	P34414 psuedomonas
5	11	31.4	5	1	UP01_MGSCU	P36639 mus muscule
6	9	25.7	4	1	ACH1_OCTM	P35904 achelonia
7	9	25.7	4	1	OCF3_OCTM	P58649 octopus aig
8	8	22.9	5	1	TRM1_PSEUT	P15673 escherichia
9	8	22.9	6	1	GIF1_MYCTH	P15736 metilus edu
10	7	20.0	3	1	THYL_PIC	P01151 sus scrofa
11	7	20.0	4	1	LCML_PSEUT	P15516 pseudomonas
12	7	20.0	4	1	TOPT_HUMAN	P31758 homo sapien
13	7	20.0	5	1	HPP3_PCTIN	P34425 bolitoglossa
14	7	20.0	5	1	E133_PCTIN	P32699 lathyrus tuc
15	7	20.0	5	1	PAP2_PARMA	P31864 paracatulus
16	7	20.0	5	1	PRC1_PERAK	P11373 periplaneta
17	7	20.0	5	1	SUSA_ACHRO	P13991 acheta domo
18	7	20.0	5	1	TPIS_CANFA	P34714 canis famli
19	7	20.0	5	1	CIF2_MYTEC	P15737 mytilus edu
20	7	20.0	6	1	E101_LITRU	P32096 littorina rub
21	7	20.0	6	1	FANP_MONEX	P41966 monodelia ex
22	7	20.0	6	1	OVN1_LSPDE	P42985 leptinotars
23	7	20.0	6	1	THOF_SABEG	P41495 saurcaphaga
24	7	20.0	6	1	VP19_HSVIK	P23210 herpes simp
25	6	17.1	3	1	GRWM_HUMAN	P31157 homo sapien
26	6	17.1	3	1	LUXE_VIBFI	P24272 vibrio fusc
27	6	17.1	4	1	EOSI_HUMAN	P02731 homo sapien
28	6	17.1	5	1	ALIA_CARMA	P31817 carcinus ma
29	6	17.1	5	1	BIOA_CITFR	P13071 citrobacter
30	6	17.1	5	1	RE11_LITRU	P30276 littorina rub
31	6	17.1	5	1	RE32_LITRU	P32073 littorina rub
32	6	17.1	6	1	ASP2_LACSN	P33655 lactobacill
33	6	17.1	6	1	LOK1_LOQMI	P41491 leccothia mli

```

RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PT OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDa.
CC STENA-20PAGE: P3605;
CC NON_TER 5
CC SEQUENCE 5 AA: 474 MW: 758A8A5AAR00000 CRC54;

Query Match 37.1%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GUT 5
DB 3 GDS 5

RESULT 3
RM01_YEAST
ID RM01_YEAST STANDARD: PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created);
DT 01-JUN-1994 (Rel. 29, Last sequence update);
DT 01-JUN-1994 (Rel. 29, Last annotation update);
DE Mitochondria; 6S ribosomal protein L1 (Yali) (Fragment);
GN MRPL1;
OS Saccharomyces cerevisiae (Baker's yeast);
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycos;
CX NCBI_TaxID=4932;
RN [1];
RP SEQUENCE.
RX MEDLINE=91285105; PubMed 2050625;
RA Gronmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reis R.S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RL subunit from yeast mitochondria.";
EL FBS Lett. 284:51-56(1992);
DR PIR: S17255; S17255;
DR SGD: L0002681; MRPL1;
FW Ribosomal protein: Mitochondrion.
KT NON_TER 4
SQ SEQUENCE 4 AA: 402 MW: 7771B2D5D06000000 CRC54;

Query Match 34.3%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TP 6
DB 3 TP 4

RESULT 4
TRPI_PSEPU
ID TRPI_PSEPU STANDARD: PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created);
DT 01-JUN-1994 (Rel. 29, Last sequence update);
DT 01-FEB-1995 (Rel. 31, Last annotation update);
DE TrpA operon transcriptional activator (Fragment);
GN TRPI;
OS Pseudomonas putida;
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas;
CX NCBI_TaxID=303;
RN [1];
RP SEQUENCE FROM N.A.
RX STRAIN=PPG1 C15;
RX MEDLINE=89335826; PubMed=2503057;
RX Eberly L., Crawford J.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT putida.";
DL Biochimie 71:521-531(1989).

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CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPA BINDS UPSTREAM OF THE
CC TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC EMBL: X13299; CAA31660.1;
CC EST: IPR000847; HRL_LYSR;
CC PROSITE: PS00044; HRL_LYSR_FAMILY; PARIAL;
CC Tryptophan biosynthesis; Transcription regulation; Activator;
CC DNA-binding.
CC NON_TER 6
CC SEQUENCE 6 AA: 683 MW: 77672AA1ED06F030 CRC54;

Query Match 34.3%; Score 12; DB 1; Length 6;
Best Local Similarity 56.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DTP 6
DB 4 DLP 6

RESULT 5
UFCL_MOUSE
ID UFCL_MOUSE STANDARD: PRT; 5 AA.
AC P36639;
DT 01-OCT-1994 (Rel. 30, Created);
DT 01-OCT-1994 (Rel. 30, Last sequence update);
DT 01-FEB-1995 (Rel. 31, Last annotation update);
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment);
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
CX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE.
RX TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RX Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RL using preparative two-dimensional gel electrophoresis.";
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PT OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
CC NON_TER 5
CC SEQUENCE 5 AA: 717 MW: 7364C87043100000 CRC54;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GR 2
DB 3 GR 4

RESULT 6
ACH1_ACHU
ID ACH1_ACHU STANDARD: PRT; 4 AA.
AC P35604;
DT 01-JUN-1994 (Rel. 29, Created);
DT 01-JUN-1994 (Rel. 29, Last sequence update);
DT 15-JUL-1998 (Rel. 36, Last annotation update);

```

DE Achatin-1.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinidae; Achatinidae; Achatina.  
OX NCBI\_TaxID=6540;  
RN [1]  
RP SEQUENCE CHARACTERIZATION AND SYNTHESIS.  
RC STRAIN=FERUSSAC; TISSUE=Gastrophys.  
RX MEDLINE=89273551; PubMed=2597281;  
RA Kamatani Y., Minakata H., Ronny P.T.M., Iwasaka T., Watanabe K.,  
RA Funase K., Sun X.P., Yotsugi A., Kim K.H., Novales-Rojas P.,  
RA Novalles E.T., Kanapi C.G., Takeuchi H., Nomoto K.,  
RA Achatin-1, an endogenous neuroexcitatory tetrapeptide from Achatina  
RT fulica Ferussac containing a D-amino acid residue.  
RL Biochem. Biophys. Res. Commun. 160:1615-1620(1989).  
RN [2]  
RN CHARACTERIZATION.  
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;  
RX MEDLINE=93014529; PubMed=1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwasaka T., Nomoto K.,  
RA "Crystal structure and molecular conformation of achatin-1  
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
RT D-amino acid residue".  
RL Int. J. Pept. Protein Res. 45:258-264(1992).  
RN [3]  
RN X-RAY CRYSTALLOGRAPHY.  
RC MEDLINE=93014529; PubMed=1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwasaka T., Nomoto K.,  
RA "Crystal structure and molecular conformation of achatin-1  
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
RT D-amino acid residue".  
RL Int. J. Pept. Protein Res. 45:258-264(1992).  
RN [4]  
RN FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
CC NEURON (PON). HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
CC HEART BEAT. ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
CC PIR; A32480; A12480.  
DR Hormone; D-amino acid.  
FT MOD\_RES 2 2 D-PHENYLALANINE.  
SQ SEQUENCE 4 AA: 408 MW: 5606959100000000 CRC64:  
Query Match 25.7%; Score 9; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GRGD 4  
DB 1 GPAD 4

RESULT 7  
OCP3\_OCTMI  
ID OCP3\_OCTMI STANDARD; PRT; 4 AA.  
AC P58649;  
DT 28-FEB-2003 (Rel. 41, Created);  
DT 28-FEB-2003 (Rel. 41, Last sequence update);  
DE Cardioactive peptides Ocp-3/Ocp-4.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=85766;  
RN [1]  
RN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10875044;  
RA Iwakoshi E., Hisada M., Minakata H.,  
RA "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor".  
RL Peptides 21:623-630(2000).  
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
QY 1 GRGD 4  
DB 1 GPAD 4

QC active than Ocp-3.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.  
CC -1- MASS SPECTROMETRY: MW=195.2; METHOD=MALDI.  
KW Hormone; D-amino acid.  
KW MOD\_RES 2 2 D-SERINE (IN OCP-4).  
SQ SEQUENCE 4 AA: 463 MW: 6061559810000000 CRC64:  
Query Match 25.7%; Score 9; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GRGD 4  
DB 1 GSWD 4

RESULT 8  
TRM3\_ECOLI  
ID TRM3\_ECOLI STANDARD; PRT; 5 AA.  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created);  
DT 01-JAN-1990 (Rel. 13, Last sequence update);  
DE TRM protein (Fragment).  
DE TRAM.  
GN TRAM.  
OS Escherichia coli.  
OC Plasmid IncFII R100.  
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC Enterobacteriaceae; Escherichia.  
CX NCBI\_TaxID=562;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=88227859; PubMed=2836343;  
RA Imamoto S., Yoshioka Y., Ohtsubo E.,  
RA "Identification and characterization of the products from the trm3  
RT and trm4 genes of plasmid R100".  
RL J. Bacteriol. 170:2749-2757(1988).  
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE TRAM FAMILY.  
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EXBL; M20941; -; NOT\_ANNOTATED\_TIS.  
LP PIR; A32014; A32014.  
KW Conjugation; Plasmid; DNA-binding.  
FT MOD\_RES 1 1  
SQ SEQUENCE 5 AA: 634 MW: 6818144435000000 CRC64:  
Query Match 22.9%; Score 8; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 RGD 4  
DB 1 KND 3

RESULT 9  
CIP1\_MYTD  
ID CIP1\_MYTD STANDARD; PRT; 6 AA.  
AC P13736;  
DT 01-JAN-1990 (Rel. 13, Created);  
DT 01-JAN-1990 (Rel. 13, Last sequence update);  
DE CIP1.  
DI 15-DEC-1998 (Rel. 37, Last annotation update)

DE Contraction-inhibiting peptide I (MIP I).  
OS *Mytilus edulis* (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6250;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Pedal ganglion;  
RX MEDLINE=86240357; PubMed=3377776;  
RA Hirata T., Kubota T., Iwasawa N., Takabatake I., Ikeda T., Mutsaers Y.,  
RT "Structures and actions of Mytilus inhibitory peptides."  
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
CC -1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SHEEP MOLLUSCAN  
MUSCLES.  
CC -1- SIMILARITY: TO MIP I2.  
DR PIR: A27696; A27696.  
KW Hormone; Amidation.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;  
Query Match 22.9%; Score 8; DB 1; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1; Gap 0;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 P 6  
DB 2 S 3  
RESULT 10  
ID THYL\_PIG STANDARD: PRT: 4 AA.  
AC P01151;  
DT 21-JUL-1986 (Rel. 01, Created)  
DI 21-JUL-1986 (Rel. 01, Last sequence update)  
DE Thyroliberin (thyrotropin-releasing hormone) (TRH) (protein).  
OS *Sus scrofa* (Pig).  
OS Ovis aries (Sheep).  
OS *Bombina orientalis* (Oriental fire-bellied toad), and  
OS *Notophthalmus viridescens* (Eastern newt) (*Triturus viridescens*).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823; 9940; 3346; 8316;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Pig; TISSUE=Hypothalamus;  
RX MEDLINE=70136150; PubMed=4984938;  
RA Nair R.M.G., Harrett J.F., Bowers C.Y., Schally A.V.;  
RT "Structure of porcine thyrotropin releasing hormone."  
RL Biochemistry 9:1103-1106(1970).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=Pig;  
RX MEDLINE=70039904; PubMed=4982117;  
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
RT "The identity of chemical and hormonal properties of the thyrotropin  
releasing hormone and pyroglutamate-histidyl-proline amide."  
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=Sheep; TISSUE=Hypothalamus;  
RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.;  
RT "The elucidation of the primary structure of the hypothalamic thyroid  
stimulating hormone releasing factor of ovine origin by means of mass  
spectrometry."  
RL Org. Mass Spectrom. 5:221-228(1971).  
RN [4]  
RP SYNTHESIS.  
RC SPECIES=Sheep;  
RX MEDLINE=70163386; PubMed=4985794;  
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.

RA Guillemin R.;  
PT "Characterization of ovine hypothalamic hypophysiotropic  
TSH-releasing factor."  
RL Nature 226:321-325(1970).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=B. orientalis; TISSUE=Skin;  
RX MEDLINE=76138399; PubMed=815011;  
RA Yasuhara T., Nakajima I.;  
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin."  
RL Chem. Pharm. Bull. 23:3301-3303(1975).  
RN [6]  
RP SEQUENCE.  
RC SPECIES=N. viridescens;  
RX MEDLINE=75035605; PubMed=4214528;  
RA Grimmel-Joergensen Y., McKelvy J.F.;  
RT "Biosynthesis of thyrotropin releasing factor by newt (*Triturus  
viridescens*) brain in vitro. Isolation and characterization of  
thyrotropin releasing factor."  
RL J. Neurochem. 23:471-478(1974).  
CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH  
IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/  
NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/  
NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
DR PIR: A5919; RHITO.  
DR PIR: A2971; A92971.  
DR PIR: A33750; RSHST.  
KW Amidation; Pyroglutamate carboxylic acid.  
FT MOD\_RES 1  
FT MOD\_RES 3  
FT MOD\_RES 3  
SQ SEQUENCE 3 AA; 360 MW; 7761F66C6C0003C0 CRC64;  
Query Match 20.0%; Score 7; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1; Gap 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 P 6  
DB 3 P 3  
RESULT 11  
ID DCM\_PSECH STANDARD: PRT: 4 AA.  
AC P19916;  
DT 31-FEB-1991 (Rel. 17, Created)  
DI 31-FEB-1991 (Rel. 17, Last sequence update)  
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
dehydrogenase subunit L) (CO-DH L) (Fragment).  
GN CUTL  
OS *Pseudomonas carboxydohydrogena*.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraat M., Hugendieck T., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydohydrogenic bacteria."  
RL Arch. Microbiol. 152:335-341(1989).  
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
dioxide.  
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced  
acceptor.  
CC -1- COFACTOR: Molybdenum (molybdopterin).  
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
SMALL.  
DR PIR: P10140; P10140.  
KW Oxidoreductase; Molybdenum.  
FT NONTER 4  
FT NONTER 4  
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0C6C0000 CRC64;

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Query Match          20.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 4 P 4

RESULT 12
TUFT_HUMAN
ID TUFT_HUMAN STANDARD: PRT: 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishida K., Constantinopoulos A., Satch P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishida K., Constantinopoulos A., Satch P.S., Najjar V.A.;
RT "The physiological role of the lymphoid leukokinin on the phagocytic
effect of leucophilic gamma globulin (leukokinin) on the phagocytic
activity of human polymorphonuclear leucocytes.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
DR PIR: A02147; A02147.
DR MM: 191150;
DR GO: GO:0003823; Phagocytosis; NAS.
DR SO: SO:0005609; Phagocytosis; NAS.
SQ SEQUENCE 4 AA: 501 MW: 7417632100000000 CRC64:

Query Match          20.0%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 3 P 3

RESULT 13
BPP7_BOTIN
ID BPP7_BOTIN STANDARD: PRT: 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
enzyme inhibitor).
OS Bothrops insularis (Island Jararaca) (Oceania Jararaca)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RX MEDLINE=90351557; PubMed=2385615;
RA Cintra A.C.O., Vieira C.A., Gallo J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1993).
CC -!- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that deactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: G37196; G37196.
DR KW Hypotensive agent; Pyrrolidone carboxylic acid.
DR FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
DR SQ SEQUENCE 5 AA: 629 MW: 7765047326000000 CRC64:

Query Match          20.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 5 P 5

RESULT 14
E103_LITRU
ID E103_LITRU STANDARD: PRT: 5 AA.
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RX MEDLINE=521639-645(1999);
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian bushing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC Amphibian defense peptide; Amidation.
DR KW RES 5 5 AMIDATION.
DR SQ SEQUENCE 5 AA: 630 MW: 6697612090000000 CRC64:

Query Match          20.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 4 P 4

RESULT 15
PAP2_PAPMA
ID PAP2_PAPMA STANDARD: PRT: 5 AA.
AC P61864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXL) (fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OC NCBI_TaxID=31087;

```

RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=1782139;  
RA Lazarovici P., Primor N., Loew L.M.;  
RI "Purification and pore-forming activity of two hydrophobic  
RT polypeptides from the secretion of the Red sea moses sole (Paralichthys  
RM marmoratus)".; 261:16704-16713(1986);  
RL J. Biol. Chem. 261:16704-16713(1986);  
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant  
CC properties. Forms voltage-dependent, ion-permeable channels  
CC in membranes. At high concentration causes cell membrane lysis.  
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PARAXIN FAMILY.  
KW Toxin.  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA: 614 MW: 776990308100000 OMC64;  
  
Query Match 20.0%; Score 7; DP 1; Length 5;  
Best Local Similarity 100.0%; Prod No. 1; 10005;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 P 6  
D0 5 P 5  
  
Search completed: September 16, 2003, 18:19:53  
Job time : 12 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw-align

Run on: September 16, 2003, 14:16:09.3 Search time 32 seconds  
(without alignments)  
46.185 Million gail updates/sec

Title: US-09-780-612A-1  
Perfect score: 35  
Sequence: 1 GRLTP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.4

- 1: sp-archaea\*
- 2: sp-bacteria\*
- 3: sp-fungi\*
- 4: sp-human\*
- 5: sp-invertebrate\*
- 6: sp-mammal\*
- 7: sp-misc\*
- 8: sp-orthocell\*
- 9: sp-phage\*
- 10: sp-plant\*
- 11: sp-rodent\*
- 12: sp-virus\*
- 13: sp-vertebrate\*
- 14: sp-unclassified\*
- 15: sp-virus\*
- 16: sp-bacteriap\*
- 17: sp-archeap\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	31.4	5	P83073	P83073 Bacillus sp.
2	7	20.0	5	P83308	P83308 Gallus gal.
3	5	14.3	6	P82181	P82181 Spinacia sp.
4	5	14.3	5	P82541	P82541 Spinacia sp.
5	5	14.3	6	P82182	P82182 Spinacia sp.
6	2	5.7	4	Q08433	Q08433 Rattus sp.
7	2	5.7	5	Q99007	Q99007 horsemul vol.

ALIGNMENTS

RESULT 1  
P83073 PRELIMINARY: PRT: 5 AA.  
ID P83073  
AC P83073;

DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE 38 kDa protein (Fragment).  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
CX NCBI\_TaxID=1396;  
RN 1;  
RP SEQUENCE  
RC STRAIN-NCIMB 11796;  
FA Browne N., Dowds B.C.A.;  
RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
FT NON\_TER 5  
SQ SEQUENCE 5 AA: 623 MW: 6861AAA46:00006 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DT 5  
LB 3 DT 4

RESULT 2  
P83308 PRELIMINARY: PRT: 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE FMRFamide-like neuropeptide (LPLRF-amide).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euarchontomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
CX NCBI\_TaxID=9031;  
RN 1;  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE=Brain;  
RX PubMed=6137771;  
FA Dockray G.J., Reeve J.R. Jr., Shively J., Sayton R.J., Barnard C.S.;  
FT \*A novel active pentapeptide from chicken brain identified by  
FT antibodies to FMRFamide\*;  
RL Nature 305:328-330(1983).  
CS -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA: 6924074767430000 CRC64;

Query Match 20.0%; Score 7; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.3e-05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6  
LB 2 P 2

RESULT 3  
P82181 PRELIMINARY: PRT: 6 AA.  
AC P82181;  
DT 01-JUN-2000 (TREMBlrel. 14, Created)  
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
DE 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
CX NCBI\_TaxID=3562;



```

>P SEQUENCE.
>R STRAIN=CV, ALVARO; TISSUE=Leaf;
>X MEDLINE=20435799; PubMed:10874046;
>A Yamaguchi K., Subramanian A.R.;
>T "The plastid ribosomal proteins. Identification of all the proteins in
>R the 50 S subunit of an organelle ribosome (chloroplast).";
>J. Biol. Chem. 275:28466-28482(2000).
>C - FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
>C - SUBCELLULAR LOCATION: CHLOROPLAST.
>C - TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
>C - MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 15.5 KDA.
>C - SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
>R InterPro: IPR001793; Ribosomal_L10.
>R InterPro: IPR002363; Ribosomal_L10sub.
>R Pfam: PF00466; Ribosomal_L10; PARTIAL.
>R PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
>R Ribosomal protein; Chloroplast; rRNA-binding.
>R NON_TER 6
>S SEQUENCE 6 AA: 675 MW: 632184156055000 CRC64;

Query Match 14.3%; Score 5; DP 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
DB 4 R 4

RESULT 4
P82541
ID P82541 PRELIMINARY: PRT: 6 AA.
AC P82541
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 36S ribosomal protein S19 beta (fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=CV, ALVARO; TISSUE=Leaf;
RX MEDLINE=20435799; PubMed:10874039;
>A Yamaguchi K., von Knoblauch K., Subramanian A.R.;
>T "The plastid ribosomal proteins. Identification of all the proteins in
>R the small subunit of an organelle ribosome (chloroplast).";
>J. Biol. Chem. 275:28455-28465(2000).
>C - FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
>C - SUBCELLULAR LOCATION: CHLOROPLAST.
>C - TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
>C - MASS SPECTROMETRY: MW:10477.0; METHOD=ELECTROSPRAY.
>C - MASS SPECTROMETRY: MW:10495; METHOD=MALDI.
>C - MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN P.I. S19 BETA
>C FORM IS THE MINOR BASIC FORM.
>C - MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
>C - SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
>R InterPro: IPR002222; Ribosomal_S19.
>R Pfam: PF00203; Ribosomal_S19; PARTIAL.
>R PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
>R PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
>R Ribosomal protein; Chloroplast; rRNA-binding.
>R NON_TER 6
>S SEQUENCE 6 AA: 732 MW: 633373544110000 CRC64;

Query Match 14.3%; Score 5; DP 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 I 5
DB 1 I 1

RESULT 5
P82182
ID P82182 PRELIMINARY: PRT: 6 AA.
AC P82182
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV, ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed:10874046;
>A Yamaguchi K., Subramanian A.R.;
>T "The plastid ribosomal proteins. Identification of all the proteins in
>R the 50 S subunit of an organelle ribosome (chloroplast).";
>J. Biol. Chem. 275:28466-28482(2000).
>C - FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
>C - SUBCELLULAR LOCATION: CHLOROPLAST.
>C - TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
>C - MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
>C - SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
>R InterPro: IPR001793; Ribosomal_L10.
>R InterPro: IPR002363; Ribosomal_L10sub.
>R Pfam: PF00466; Ribosomal_L10; PARTIAL.
>R PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
>R Ribosomal protein; Chloroplast; rRNA-binding.
>R NON_TER 6
>S SEQUENCE 6 AA: 675 MW: 632184156055000 CRC64;

Query Match 14.3%; Score 5; DP 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
DB 4 R 4

RESULT 6
Q08433
ID Q08433 PRELIMINARY: PRT: 4 AA.
AC Q08433
DT 03-NOV-1996 (TrEMBLrel. 01, Created)
DT 03-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed:1840486;
>A Sato H., Aono S., Kashiwamata S., Kawai O.;
>T "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
>R hyperbilirubinemic Gunn rat.";
>R. J. Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
>R EMBL: S38636; AAB19259.1; .
>R NON_TER 4
>S SEQUENCE 4 AA: 473 MW: 633732042000000 CRC64;

```

Query Match 5.7% Score 2: DB 10 Length 5;  
 Best Local Similarity 0.0% Pred. NO. 8.3e-05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
 :  
 Db 4 K 4

RESULT 7  
 Q59007 PRELIMINARY: ERT: 5 AA;  
 ID Q99007  
 AC Q99007;  
 DT 01-NOV-1996 (TREMUREL\_01, Created)  
 DT 01-NOV-1996 (TREMUREL\_01, Last sequence update)  
 DT 01-MAR-2003 (TREMUREL\_24, Last annotation update)  
 DE Alpha amylase (Fragment);  
 GN AMY1 GENE;  
 OS Hordeum vulgare (Barley);  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum;  
 CX NCBI\_TaxID:4513;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:91329704; PubMed:1831055;  
 RA Jacobsen J.V., Close T.J.;  
 RT \*Control of transient expression of chimaeric genes by gibberellic  
 RT acid and abscisic acid in protoplasts prepared from mature barley  
 RT aleurone layers.\*;  
 RL Plant Mol. Biol. 16:713-721(1991).  
 DR EMBL: X54643; CAA38455.1; -;  
 FT NON-ITER 5  
 SQ SEQUENCE 5 AA; 60C MW; 51E3344DD6F00009 CRC64;

Query Match 5.7% Score 2: DB 10 Length 5;  
 Best Local Similarity 0.0% Pred. NO. 8.3e-05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
 :  
 Db 4 K 4

Search completed: September 16, 2003, 18:20:37  
 Job time : 32 secs

GenCore version 5.1.5  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 18:11:12 : Search time 41 seconds  
(without alignments)  
23,228 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35  
Sequence: 1 GRCDFP 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107963 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
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- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	35	100.0	6	AA196709	Adhesion formation
2	35	100.0	6	AA197384	PR-39 beta disintegrin
3	35	100.0	6	AA197440	Synthetic, peptide
4	35	100.0	6	AA194571	RGD peptide, synthetic
5	35	100.0	6	AA195314	Neutrophil-activating
6	35	100.0	6	AA191127	Non-crosslinked fibrin
7	35	100.0	6	AA11025	Non-crosslinked fibrin
8	35	100.0	6	AA194459	RGD peptide that is
9	35	100.0	6	AA1928163	Peptide #3 used to

10	35	100.0	6	21	AA190475	Cell adhesion pept
11	35	100.0	6	22	AA191572	Fibronectin fragme
12	35	100.0	6	23	AA190976	Integrin modulator
13	35	100.0	9	18	AA15667	Platelet aggregati
14	35	100.0	9	23	AA161362	Anti-thrombotic cy
15	35	100.0	9	23	AA161364	Interferin-binding p
16	35	100.0	10	18	AA15655	Platelet aggregati
17	35	100.0	10	18	AA15656	Platelet aggregati
18	35	100.0	10	18	AA15657	Platelet aggregati
19	35	100.0	10	18	AA15658	Platelet aggregati
20	35	100.0	10	18	AA15659	Platelet aggregati
21	35	100.0	10	18	AA15663	Platelet aggregati
22	35	100.0	10	18	AA15670	Platelet aggregati
23	35	100.0	10	23	AA161294	Anti-thrombotic cy
24	35	100.0	10	23	AA161350	Anti-thrombotic cy
25	35	100.0	10	23	AA161351	Anti-thrombotic cy
26	35	100.0	10	23	AA161352	Anti-thrombotic cy
27	35	100.0	10	23	AA161353	Anti-thrombotic cy
28	35	100.0	10	23	AA161354	Anti-thrombotic cy
29	35	100.0	10	23	AA161358	Anti-thrombotic cy
30	35	100.0	10	23	AA161358	Anti-thrombotic cy
31	35	100.0	10	23	AA161358	Anti-thrombotic cy
32	35	100.0	493	22	AA161360	Human intracellular
33	35	100.0	897	24	AA161371	H. influenzae BASB
34	35	100.0	899	24	AA161372	H. influenzae BASB
35	35	100.0	1005	21	AA161383	Haemophilus influe
36	35	100.0	1011	21	AA161383	Haemophilus influe
37	35	100.0	1306	22	AA161381	Human intracellular
38	32	91.4	455	21	AA161391	Arabisopsis thalia
39	32	91.4	455	21	AA161391	Arabisopsis thalia
40	32	91.4	458	21	AA161390	Arabisopsis thalia
41	32	91.4	458	21	AA161390	Arabisopsis thalia
42	32	91.4	1425	22	AA161344	Novel human diagno
43	31	88.6	6	11	AA161312	Antiviral agent
44	31	88.6	6	11	AA161312	Fibronectin derive
45	31	88.6	6	13	AA161363	Peptide contg. RGD

ALIGNMENTS

RESULT 1  
AA196709  
IL AAR36709 standard; peptide; 6 AA.  
XX  
XX AAR36709;  
XX  
XX  
DT 25-MAR-2003 (updated)  
DT 26-APR-1993 (first entry)  
XX  
XX  
DE Adhesion formation prevention RGD-contig. peptide.  
XX  
XX  
XX Tissue repair; peritoneum; surgery; post-surgically; inhibition;  
XX Platelet aggregation; cardiovascular; orthopedic; thoracic;  
XX ophthalmic; CNS; use.  
XX Synthetic.  
XX  
XX WQ9305818-A1.  
XX  
XX  
PD 13-MAY-1993.  
XX  
XX  
XX 05-NOV-1992; 92WO-0509494.  
XX  
XX  
XX 07-NOV-1991; 91US-0789231.  
XX  
XX {UYSC-} UNIV SOUTHERN CALIFORNIA.  
XX  
XX RGD peptide, syn.  
XX Neutrophil-activa  
XX Non-crosslinked fi  
XX Non-crosslinked fi  
XX RGD peptide that s  
XX Peptide #3 used to

Prevention of adhesion formation, partic. post-surgically - comprises

PT administering a RGD-contg. peptide for a time sufficient to permit  
 PT tissue repair

XX Example; Page 18; 22pp; English.

XX The sequence is that of an RGD-contg. peptide which is used in a  
 CC method for prevention of adhesion formation for a time sufficient  
 CC to permit tissue repair. The method is used for minimising or  
 CC preventing adhesion formation, partic. in the peritoneum following  
 CC surgery, but also for e.g. cardiovascular, orthopaedic, thoracic,  
 CC ophthalmic, CNS and other uses. In addn., the peptide inhibits  
 CC platelet aggregation and does not induce inflammation or trauma  
 CC at the site of administration.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DA 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 L I I I I  
 Db 1 GRGDTF 6

RESULT 2  
 AAR47384  
 ID AAR47384 standard; Protein; 6 AA.

XX AAR47384;  
 AC  
 CC 25-MAR-2003 (updated)  
 DT 22-JUN-1994 (first entry)  
 DE PH-30 beta disintegrin control peptide.

XX PH-20; PH-30; contraceptive; fertilisation; sperm surface protein;  
 KW vaccine; sperm-egg fusion.

XX Rubella virus.

XX WO9325233-A1.

XX 23-DEC-1993.

XX 10-JUN-1993; 93WO-0505640.

XX 12-JUN-1992; 92US-0897383.

XX (UYCO-) UNIV CONNECTICUT.

XX Myles DG, Primakoff P;

XX WPI; 1994-007200/01.

XX Contraceptive vaccine for reducing sperm-egg fusion - comprises  
 PT peptide from sperm surface protein which stimulates antibody  
 PT prodn.

XX Example 7; Page 27; 79pp; English.

XX Example 7 describes the use of PH-30 beta disintegrin peptides  
 CC as inhibitors of sperm fusion to egg plasma membrane.  
 CC Modified peptides AAR47382-83 and control peptides (AAR47384-85)  
 CC were tested. From observations it was concluded that the  
 CC PH-30 beta disintegrin domain represents an epitope which  
 CC is critical in sperm-egg fusion.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 15; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 L I I I I  
 Db 1 GRGDTF 6

RESULT 3

AAW07430  
 ID AAW07430 standard; peptide; 6 AA.

XX AAW07430;

XX 25-MAR-2003 (updated)

DT 21-JAN-1997 (first entry)

XX Synthetic, preferred tumour invasion-inhibitory peptide.

XX Tumour invasion; extracellular matrix; ECM; metastasis; RGD sequence;  
 KW cancer; inhibition; control.

XX Synthetic.

XX US5547336-A.

XX 20-AUG-1996.

XX 17-DEC-1993; 93US-0169743.

XX 17-DEC-1993; 93US-0169743.

XX 22-NOV-1983; 83US-0554821.

XX 17-JUN-1985; 85US-0744961.

XX 16-MAR-1988; 88US-0166530.

XX 09-SEP-1988; 88US-0242713.

XX 25-FEB-1991; 91US-0660524.

XX 10-APR-1991; 91US-0683585.

XX 05-OCT-1991; 91US-0773105.

XX 19-JUN-1992; 92US-0902742.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Gehlsen KR, Pierschbacher MD, Ruoslahti E;

XX WPI; 1996-392651/39.

XX Inhibiting tumour cell invasion through an extracellular matrix -  
 PT using peptide contg. the RGD sequence, partic. for preventing tumour  
 PT metastasis  
 XX Claim 2; Column 7-8; 8pp; English.

XX AAW07430 is a preferred peptide identified in an assay for testing

XX peptides for tumour-invasion inhibitory activity. The peptides

XX (contg. the RGD sequence) shows significant inhibition of tumour

XX invasion of the ECM. Other peptides tested (see AAW07431-W06433) did

XX show inhibitory activity but to a lesser extent than peptide AAW07430

XX The peptides identified can be used to treat cancer and to prevent

XX metastasis, in partic. invasion of the extracellular matrix (ECM).

XX The peptides are soluble.

XX (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 17; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 L I I I I  
 Db 1 GRGDTF 6

```

RESULT 4
AAR94571
ID AAR94571 standard; Peptide: 6 AA.
XX AC AAR94571:
XX DT 21-JUN-1996 (first entry)
XX DE RGD peptide.
XX KW Cytotactin; neuron; neurite; cell attachment; cell elongation;
XX KW antibody.
XX OS Synthetic.
XX PN W09608513-A1.
XX PD 21-MAR-1996.
XX PF 14-SEP-1995; 95WO-US11684.
XX PR 16-SEP-1994; 94US-C308359.
XX PA (SCR1 ) SCRIPPS RES INST.
XX PI Crossin KL, Phillips G, Prieto AL;
XX DR WPI; 1995-179904/18.
XX PT Cytotactin polypeptide(s), derivs. and antibodies - capable of
XX PT stimulating neuronal cell attachment, neurite out-growth and cell
XX PT elongation
XX PS Example 5: Page 81; 159pp; English.
XX CC RGD peptides (AAR94570 and AAR94571), inhibitors of cell attachment to
XX CC type I collagen, inhibited attachment of chicken fibroblasts to
XX CC cytotactin (see also AAR94547-48) by 75% and 70% respectively.
XX CC Inhibition was total when the peptides were used together with CG22,
XX CC a function-blocking monoclonal antibody against the beta-1 integrin.
XX CC This suggests that there are 2 integrin binding sites on cytotactin.
XX SQ Sequence 6 AA.
Query Match 100.0%; Score 45; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GRGDTP 6
DB 1 GRGDTP 6
RESULT 5
AAY50314
ID AAY50314 standard; Peptide: 6 AA.
XX AC AAY50314:
XX DT 12-JAN-2000 (first entry)
XX DE Neutrophil-activating pancreatic derived peptide 114.
XX KW Cell activation; pancreas; treatment; cardiovascular disease; trauma;
XX KW inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke;
XX KW organ rejection; ischemia; Alzheimer's disease; myocardial infarction;
XX KW haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina;
XX KW trauma; protease inhibitor; hypertension; sepsis.
XX OS Unidentified.
XX PN W09946367-A2.
XX PD 14-SEP-1999.
XX PF 11-MAR-1999; 99WO-US05247.
XX PR 11-MAR-1996; 98US-C036644.
XX PA (CELL-) CELL ACTIVATION INST.
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (SCR1 ) SCRIPPS RES INST.
XX PF Stoughton KB, Schmid-Schonbein GW, Hall TE, Kistler E;
XX PF WPI; 1999-580234/49.
XX PT Use of cell activating compositions in developing products for
XX PT diagnosis and treatment of e.g. cardiovascular, inflammatory,
XX PT autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
XX PT diabetes, stroke or ischemia.
XX PS Example 9: Page 184; 164pp; English.
XX CC This invention describes a novel method for the use and preparation of
XX CC cell activating compositions which involves preparing a cell activating
XX CC composition comprising (a) homogenizing pericardiac tissue in buffer at
XX CC about neutral or higher pH to produce a homogenate; (b) removing
XX CC particulates from the homogenate; (c) optionally incubating the
XX CC resulting homogenate, with particulates removed, with a protease; and
XX CC (d) fractionating the homogenate and selecting fractions that exhibit
XX CC cell activation activity. The methods can be used for improving
XX CC treatment outcome or reducing risk of treatment of e.g. cardiovascular
XX CC disease, inflammatory disease, trauma, autoimmune diseases, arthritis,
XX CC organ rejection, diabetes and diabetic complications, stroke, ischemia,
XX CC Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic
XX CC retinopathy, diabetes, venous insufficiency, unstable angina or trauma.
XX CC They can be used in the veterinary treatment of a non-human subject.
XX CC Protease inhibitors can be used to lower cell activation resulting from
XX CC these diseases and deficiencies. The detection of an elevated level of
XX CC hydrogen peroxide can be used to detect an inflammatory condition. An
XX CC elevated level of hydrogen peroxide in plasma or whole blood and in the
XX CC presence of superoxide dismutase (SOD) indicates leukocyte up
XX CC regulation, e.g. indicative of the onset of an acute cardiovascular
XX CC disorders, such as disease onset or ischemic complications. An elevated
XX CC level of hydrogen peroxide in plasma or whole blood and a low level in
XX CC the presence of SOD is indicative of a chronic or immune compromised
XX CC condition e.g. hypertension or sepsis. AAY50201-Y50334 represent peptides
XX CC used in the method of the invention.
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GRGDTP 6
DB 1 GRGDTP 6
RESULT 6
AAY31127
ID AAY31127 standard; peptide: 6 AA.
XX AC AAY31127:
XX DT 21-OCT-1999 (first entry)
XX DE Non-crosslinked protein particle peptide 176.
XX KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
XX KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX OS Synthetic.
XX PN

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PN US5945033-A.  
 XX 31-AUG-1999.  
 XX 12-NOV-1996; 96US-0747137.  
 XX 14-MAR-1994; 94US-0212546.  
 PR 15-JAN-1991; 91US-0641720.  
 PR 13-OCT-1992; 92US-0959560.  
 PR 01-JUN-1993; 93US-0069831.  
 PR 12-NOV-1996; 96US-0747137.  
 XX (HEMO-) HEMOSPHERE INC.  
 PA Yen RCK:  
 PI WPI: 1999-508153/42.  
 XX Non-crosslinked protein particles for therapeutic and diagnostic use  
 PT Example 22; Column 123-124; 65pp; English.  
 PS This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which  
 CC is stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention.  
 XX Sequence 6 AA:  
 SQ

Query Match 100.0%; Score 45; PR 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 GKGDTF 6  
 II I I  
 Db 1 GKGDTF 6

RESULT 7  
 AAY31025  
 ID AAY31025 standard; peptide: 6 AA.  
 AC AAY31025;  
 XX 21-OCT-1999 (first entry)  
 DT Non-crosslinked protein particle peptide 74.  
 DE Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 KW albumin; haemoglobin; nanometer; micrometer; clearance.  
 XX Synthetic.  
 OS US5945033-A.  
 XX 31-AUG-1999.  
 PD 12-NOV-1996; 96US-0747137.  
 PF 14-MAR-1994; 94US-0212546.  
 PR 15-JAN-1991; 91US-0641720.  
 PR 13-OCT-1992; 92US-0959560.  
 PR 01-JUN-1993; 93US-0069831.

PR 12-NOV-1996; 96US-0747137.  
 XX (HEMO-) HEMOSPHERE INC.  
 PA Yen RCK:  
 PI WPI: 1999-508153/42.  
 XX Non-crosslinked protein particles for therapeutic and diagnostic use  
 PT Example 22; Column 81-82; 65pp; English.  
 PS This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which  
 CC is stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention.  
 XX Sequence 6 AA:  
 SQ

Query Match 100.0%; Score 45; PR 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 GKGDTF 6  
 II I I  
 Db 1 GKGDTF 6

RESULT 6  
 AAY84459  
 ID AAY84459 standard; Peptide: 6 AA.  
 AC AAY84459;  
 XX 25-MAR-1999 (first entry)  
 DT RGE peptide that stimulates cell invasion by S. pyogenes 90-226.  
 DE Streptococcus pyogenes 90-226; pathogen; inhibitor;  
 KW cell adhesion; cell invasion; treatment; bacterial infection;  
 XX fungal infection.  
 OS Synthetic.  
 XX WO9856408-A2.  
 PN 17-DEC-1998.  
 DE 10-JUN-1998; 98WO-0512019.  
 PF 10-JUN-1997; 97US-0049124.  
 PR (MINU) UNIV MINNESOTA.  
 XX Cleary PF, Cue DR;  
 PI WPI: 1999-080856/07.  
 XX Method for treating mammal infected by pathogenic microorganism -  
 PT comprises administering to mammal composition comprising inhibitory  
 PT compound which inhibits adherence to or invasion of a cell by  
 PT microorganism  
 XX

PS Example 2; Page 43; 89pp; English.

XX The present sequence represents a RGD peptide that is able to  
CC stimulate cell invasion by *Streptococcus pyogenes* 50-226. The  
CC peptides were used in the course of the invention. The  
CC specification describes the treatment of a mammary infected  
CC by a pathogenic microorganism which comprises administering an  
CC inhibitory compound to inhibit adherence to or invasion of cells  
CC by the pathogen. The method is used in the treatment of bacteria,  
CC or fungal infection.

XX Sequence 6 AA;  
SQ Query Match 100.0%; Score 35; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9, 9e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
Db 1 GRGDTP 6

RESULT 9

AA28163  
ID AAB28163 standard; peptide: 6 AA.

AC AAB28163;

DT 09-FEB-2001 (first entry)

XX Peptide #3 used to assay vitronectin receptor binding inhibition.

XX Antiviral; antiinflammatory; cytostatic; vasotropic; antirheumatic;  
KW antiarthritic; ophthalmological; osteopathic;  
KW amido-carboxylic acid derivative; cancer; angiogenesis;  
KW neovascularisation; macular degeneration; glaucoma; blindness  
KW rheumatoid arthritis; restenosis; viral infection; bone resorption;  
KW osteoporosis; osteopenia; periodontal disease; hyperparathyroidism;  
KW Paget's disease; integrin vitronectin receptor; alpha\_vbeta\_3; melanoma.

XX Unidentified.

XX WO200061545-A1.

XX 19-OCT-2000.

XX 13-APR-2000; 2000W-US17027.

XX 14-APR-1999; 9902-0291470.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Gopalasamy A, Yang HY;

XX WPI: 2000-687029/w7.

XX New amido-carboxylic acid derivatives are integrin inhibitors used for  
PT treating e.g. cancer, restenosis, osteoporosis, viral infection and  
PT bone disease.

XX Disclosure: Page 17; 67pp; English.

XX The present invention relates to amido-carboxylic acid derivatives. The  
CC amido-carboxylic acid derivatives may be used for treating cancer,  
CC angiogenesis, neovascularisation, macular degeneration, glaucoma,  
CC blindness, rheumatoid arthritis, restenosis, smooth cell proliferation,  
CC and migration, vascular endothelial cell proliferation and migration,  
CC viral infection (characterised by bone resorption of mineralised  
CC tissues), osteoporosis, hypercalcaemia of malignancy, osteopenia due to  
CC bone metastasis, periodontal disease, hyperparathyroidism, periarthritic  
CC erosions in rheumatoid arthritis, Paget's disease, immobilisation-induced  
CC osteopenia or glucocorticoid treatment, or diseases characterised by some  
CC resorption of mineralised tissues. The present sequence is a peptide,

CC which was used as a reference compound in an assay for the ability of the  
CC amido-carboxylic acid derivatives of the present invention to inhibit  
CC integrin vitronectin receptor (alpha\_vbeta\_3) binding. Integrin  
CC alpha\_vbeta\_3 has been shown to mediate the invasion of cancerous  
CC melanoma cells into healthy tissue and to protect these cells against  
CC apoptosis. In addition, vitronectin receptor antagonists have been shown  
CC to inhibit the growth of various solid tumours of human origin.

XX Sequence 6 AA;

XX Query Match 100.0%; Score 35; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9, 9e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
Db 1 GRGDTP 6

RESULT 10

AA280475

XX AA280475 standard; peptide: 6 AA.

AC AA280475;

DT 06-JUN-2000 (first entry)

XX Cell adhesion peptide #10.

XX Bone regenerative; osteopathic; osseous tissue; reconstitution;  
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;  
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.

XX Synthetic.

XX WO2000004941-A1.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-US16803.

XX 24-JUL-1998; 98US-0122346.

XX (PEAR-) PHARMACAL BIOTECHNOLOGIES INC.

XX Budny JA;

XX WPI: 2000-195084/17.

XX System for reconstructing osseous tissue, useful e.g. for treating  
PT fractures, comprises scaffold containing promoter of bone formation and  
PT inhibitor of bone resorption.

XX Claim 14; Page 31; 44pp; English.

XX The invention relates to a novel system for reconstitution of osseous  
CC tissue comprising a scaffold carrying a compound (I) that promotes  
CC bone formation and a component that decreases bone resorption (II).  
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and  
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular  
CC matrix. (I) is preferably selected from: secretin or secretin binding  
CC fragments, proteins and peptides that facilitate cell adhesion,  
CC plasminogen activator inhibitors, protease inhibitors and  
CC metalloprotease inhibitors. The peptides AA280466-Y80492 are claimed  
CC examples of cell adhesion peptides used in the system of the invention.  
CC The system is used to replace, remodel or correct bone defects, e.g.  
CC fractures, fissures or bone mass loss. Incorporation of (I) into the  
CC scaffold results in rapid seeding by osteoblasts and the development of  
CC an organic matrix, i.e. the preformed scaffold replaces the  
CC rate-determining step of extracellular matrix formation. The scaffold can  
CC be designed to have a predetermined resorption/degradation rate, and may  
CC include regulatory compounds for specific cell types.

Sequence 6 AA:  
Query Match 100.0%; Score 35; Db 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
DB 1 GRGDP 6

RESULT 11  
ID AAB91972 standard; Peptide: 6 AA.  
XX AC AAB91972;  
DT 22-JUN-2002 (first entry)  
DE XX  
XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1146.  
XX Protection: endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification: succinimide; maleimido group; amine;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX WO200059900-A2.  
XX 23-NOV-2000.  
XX 17-MAY-2000; 2000W9-0514576.  
XX 17-MAY-1999; 540S-0134406.  
PR 10-SEP-1999; 540S-0153406.  
PR 15-OCT-1999; 990S-0159783.  
XX (CONC-) CONJUCHEM INC.  
XX PA  
XX Bridon DP, Ezrin AM, Walzer PG, Holmes DL, Imbaudeat K;  
PI WPI: 2001-112059/12.  
XX  
XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity  
PT  
PT  
PS Disclosure; Page 571; 73pp; English.  
XX  
XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (II) and a  
CC reactive group (III) (e.g. succinimide) and maleimide groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxy/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 6 AA:  
Query Match 100.0%; Score 35; Db 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
DB 1 GRGDP 6

RESULT 12  
ID ABB80076 standard; peptide: 6 AA.  
XX AC ABB80076;  
XX 27-AUG-2002 (first entry)  
DE XX  
XX Integrin modulator peptide #3.  
XX Neurodegenerative disease; amyloid; neuroprotective; anti-Alzheimer's;  
KW Alzheimer's disease; integrin; therapeutic agent.  
XX Unidentified.  
XX WC200226107-A2.  
XX 04-APR-2002.  
XX 25-SEP-2001; 2001W0-US29789.  
XX 25-SEP-2000; 2000US-235374P.  
XX (RENC) UNIV CALIFORNIA.  
XX Ignotz G, Xiaoning B, Gall CM;  
XX WFI: 2802-416420/44.  
XX Experimental models for studying neurodegenerative diseases associated  
PT with amyloid accumulation, useful for studying e.g. Alzheimer's disease  
PT and for identifying potential therapeutic agents -  
XX  
XX Claim 15: Page 63; 80pp; English.  
XX The invention relates to experimental models for studying  
CC neurodegenerative diseases associated with amyloid accumulation. The  
CC activity of peptides of the invention may be described as neuroprotective  
CC and anti-Alzheimer's. They act by inhibiting amyloid accumulation. The  
CC experimental model may be used to study neurodegenerative diseases  
CC associated with amyloid accumulation, e.g. Alzheimer's disease and to  
CC identify potential therapeutic agents for treating these diseases. The  
CC current sequence represents an integrin modulator peptide of the  
CC invention.  
XX  
XX Sequence 6 AA:  
Query Match 100.0%; Score 35; Db 24; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
DB 1 GRGDP 6

RESULT 13  
ID AAW15667 standard; peptide: 9 AA.  
XX AC AAW15667;  
XX 25-MAR-2003 (updated)  
DT 11-JUN-1997 (first entry)  
XX  
XX Platelet aggregation inhibitor #92.  
XX



KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;  
 KW hydrophobically enhanced analogue; blood platelet; endothelial surface;  
 KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;  
 KW plasma membrane; thrombosis; cell adhesion; receptor; fibronectin;  
 KW vitronectin receptor; vascular graft occlusion; therapy.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT Modified-site

FT Key

FT /note "forms peptide tend to create cyclic peptide"

FT Modified-site

FT /label OTHER

FT /note "beta1, beta-pentamethylene-histaminoacetylpeptide of beta1

FT acid"

US5612311-A.

18-MAR-1997.

22-DEC-1994.

94US-0363963.

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KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;  
 KW hydrophobically enhanced analogue; blood platelet; endothelial surface;  
 KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;  
 KW plasma membrane; thrombosis; cell adhesion; receptor; fibronectin;  
 KW vitronectin receptor; vascular graft occlusion; therapy.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT Modified-site

FT Key

FT /note "forms peptide tend to create cyclic peptide"

FT Modified-site

FT /label OTHER

FT /note "beta1, beta-pentamethylene-histaminoacetylpeptide of beta1

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US5612311-A.

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22-DEC-1994.

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KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;  
 KW hydrophobically enhanced analogue; blood platelet; endothelial surface;  
 KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;  
 KW plasma membrane; thrombosis; cell adhesion; receptor; fibronectin;  
 KW vitronectin receptor; vascular graft occlusion; therapy.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT Modified-site

FT Key

FT /note "forms peptide tend to create cyclic peptide"

FT Modified-site

FT /label OTHER

FT /note "beta1, beta-pentamethylene-histaminoacetylpeptide of beta1

FT acid"

US5612311-A.

18-MAR-1997.

22-DEC-1994.

94US-0363963.

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KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;  
 KW hydrophobically enhanced analogue; blood platelet; endothelial surface;  
 KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;  
 KW plasma membrane; thrombosis; cell adhesion; receptor; fibronectin;  
 KW vitronectin receptor; vascular graft occlusion; therapy.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT Modified-site

FT Key

FT /note "forms peptide tend to create cyclic peptide"

FT Modified-site

FT /label OTHER

FT /note "beta1, beta-pentamethylene-histaminoacetylpeptide of beta1

FT acid"

US5612311-A.

18-MAR-1997.

22-DEC-1994.

94US-0363963.

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KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;  
 KW hydrophobically enhanced analogue; blood platelet; endothelial surface;  
 KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;  
 KW plasma membrane; thrombosis; cell adhesion; receptor; fibronectin;  
 KW vitronectin receptor; vascular graft occlusion; therapy.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT Modified-site

FT Key

FT /note "forms peptide tend to create cyclic peptide"

FT Modified-site

FT /label OTHER

FT /note "beta1, beta-pentamethylene-histaminoacetylpeptide of beta1

FT acid"

US5612311-A.

18-MAR-1997.

22-DEC-1994.

94US-0363963.

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KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;  
 KW hydrophobically enhanced analogue; blood platelet; endothelial surface;  
 KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;  
 KW plasma membrane; thrombosis; cell adhesion; receptor; fibronectin;  
 KW vitronectin receptor; vascular graft occlusion; therapy.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT Modified-site

FT Key

FT /note "forms peptide tend to create cyclic peptide"

FT Modified-site

FT /label OTHER

FT /note "beta1, beta-pentamethylene-histaminoacetylpeptide of beta1

FT acid"

US5612311-A.

18-MAR-1997.

22-DEC-1994.

94US-0363963.

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XX Integrin-binding peptide.  
DE  
XX  
XX Embolisation therapy; angiogenic-dependant diseases; cancer;  
KW drug delivery; vaccine; microsphere; precancerous; therapeutic factor;  
KW integrin-binding; cytostatic.  
XX  
XX  
OS Unidentified.  
XX  
XX WO200172281-A2.  
FN  
XX  
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PD 04-OCI-2001.  
XX  
XX 23-MAR-2001; 2001WO-US03619.  
XX  
XX 24-MAR-2000; 2000US-191899P.  
PR  
XX (BIOS-) BIOSPHERE MEDICAL INC.  
PA  
XX  
XX Vogel J, Boschetti E;  
PI  
XX  
XX WPI; 2002-034141/G4.  
DR  
XX  
XX  
PS Microspheres for active embolisation comprising a cross linked  
PT hydrophilic polymer and a drug or vaccine are useful for site-directed  
PT therapy via the blood supply, particularly of tumours -  
XX  
XX Disclosure; Page 34; 73pp; English.  
XX  
XX The invention relates to a microsphere suitable for active embolisation,  
CC comprising a biocompatible, cross-linked and substantially hydrophilic  
CC polymer and a drug or vaccine, the activity of which may be described as  
CC cytostatic. Compositions and methods of the invention may be used in the  
CC treatment of angiogenic-dependant diseases including cancer and  
CC precancerous disorders. The microspheres are used for site directed  
CC delivery of therapeutic drugs, pharmaceuticals or vaccines, particularly  
CC for treatment of tumours. The current sequence represents an integral  
CC binding peptide that may be used as a transfection agent to increase the  
CC efficiency of transfer of a bioactive therapeutic factor into cells.  
XX  
XX  
50 Sequence 9 AA:

Query Match 100.0%; Score 45; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GRGDTP 5  
Db 4 GRGDTP 9  
|||||

Search completed: September 16, 2003, 14:15:41  
Job time : 42 secs

bioinformatics version 5.1.6  
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OM protein - Protein search, using sw model

Run on: September 16, 2003, 18:15:57 : Search time 16 seconds  
(without alignments)  
15,467 Million comparisons/sec

Title: US-09-780-612A-1

Perfect score: 35  
Sequence: 1 GRGDTP 4

Scoring table: PLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 9

Maximum DB seq length: 209000000

Post-processing: Minimum Match on  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_patents\_AA:\*

- 1: /cgn2.6/plodata/1/aa/7A\_COMB.pep:\*
- 2: /cgn2.6/plodata/1/aa/7B\_COMB.pep:\*
- 3: /cgn2.6/plodata/1/aa/6A\_COMB.pep:\*
- 4: /cgn2.6/plodata/1/aa/6B\_COMB.pep:\*
- 5: /cgn2.6/plodata/1/aa/PCIS\_COMB.pep:\*
- 6: /cgn2.6/plodata/1/aa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	1 US-08-169-743-2	Sequence 2, Appl
2	35	100.0	6	1 US-08-178-482-7	Sequence 7, Appl
3	35	100.0	6	1 US-08-234-597-1	Sequence 1, Appl
4	35	100.0	6	2 US-08-747-137-74	Sequence 74, Appl
5	35	100.0	6	2 US-08-747-137-175	Sequence 176, Appl
6	35	100.0	6	3 US-08-956-699-1	Sequence 1, Appl
7	35	100.0	6	4 US-09-606-473-1	Sequence 1, Appl
8	35	100.0	6	4 US-09-485-653-1	Sequence 1, Appl
9	35	100.0	6	4 US-09-548-697A-2	Sequence 2, Appl
10	35	100.0	6	5 PC-US33-05640-45	Sequence 45, Appl
11	35	100.0	9	4 US-08-445-745-114	Sequence 114, Appl
12	35	100.0	9	4 US-08-456-745-92	Sequence 92, Appl
13	35	100.0	9	4 US-08-445-638-114	Sequence 114, Appl
14	35	100.0	10	1 US-08-445-745-50	Sequence 50, Appl
15	35	100.0	10	1 US-08-445-745-51	Sequence 51, Appl
16	35	100.0	10	1 US-08-445-745-102	Sequence 102, Appl
17	35	100.0	10	1 US-08-445-745-103	Sequence 103, Appl
18	35	100.0	10	1 US-08-445-745-104	Sequence 104, Appl
19	35	100.0	10	1 US-08-445-745-105	Sequence 105, Appl
20	35	100.0	10	1 US-08-445-745-106	Sequence 106, Appl
21	35	100.0	10	1 US-08-445-745-110	Sequence 110, Appl
22	35	100.0	10	1 US-08-445-745-117	Sequence 117, Appl
23	35	100.0	10	4 US-08-456-466-24	Sequence 24, Appl
24	35	100.0	10	4 US-08-456-466-80	Sequence 80, Appl
25	35	100.0	10	4 US-08-456-466-81	Sequence 81, Appl
26	35	100.0	10	4 US-08-456-466-82	Sequence 82, Appl
27	35	100.0	10	4 US-08-456-466-83	Sequence 83, Appl

Sequence 84, Appl  
Sequence 88, Appl  
Sequence 95, Appl  
Sequence 50, Appl  
Sequence 51, Appl  
Sequence 102, Appl  
Sequence 103, Appl  
Sequence 104, Appl  
Sequence 105, Appl  
Sequence 106, Appl  
Sequence 110, Appl  
Sequence 117, Appl  
Sequence 12, Appl  
Sequence 41, Appl  
Sequence 39, Appl  
Sequence 13, Appl  
Sequence 46, Appl

ALIGNMENTS

Result 1  
US-08-169-743-2  
Sequence 2, Application US/08.69743  
Patent No. 5547936  
GENERAL INFORMATION:  
APPLICANT: RUOSLAHTI, ERKKI I.  
APPLICANT: PIERSCHBACHER, MICHAEL D.  
APPLICANT: GEHLEN, KURT R.  
TITLE OF INVENTION: INHIBITION OF CRIM. MIGRATION WITH  
TITLE OF INVENTION: SYNTHETIC PEPTIDES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
STREET: 444 SOUTH FLOWER STREET, SUITE 2000  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/169,743  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 07/773,106  
FILING DATE: 08-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWN, THERESA A.  
REGISTRATION NUMBER: 32,547  
REFERENCE/DOCKET NUMBER: P319102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-9949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-169-743-2

Query Match 100.0%, Score 35, DB 1, Length 6

Best Local Similarity 100.0%, Pred. No. 2.5e+05, Indels 0, Gaps 0,  
Matches 6, Conservative 0, Mismatches 0

QY 1 GRGDTP 6  
|||||

Db 1 GRGDTF 6

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RESULT 2
US-08-178-482-7
Sequence 7, Application US/08178482
Patent No. 5629294
GENERAL INFORMATION:
APPLICANT: DIERCKA, GREG S
APPLICANT: ROGERS, KATHLEEN E
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTING
TITLE OF INVENTION: ADHESION FORMATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBBINS, DALGARN, BERLINER & CARSON
STREET: 201 NORTH FIGUEROA STREET, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,482
FILING DATE: 06-JAN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,211
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: SPITALS, JOHN P
REGISTRATION NUMBER: 23,215
REFERENCE/DOCKET NUMBER: 2520-3-4
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-178-482-7

Query Match 100.0% Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2,564,051;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDTF 6
Db 1 GRGDTF 6

RESULT 3
US-08-234-997-1
Sequence 1, Application US/08234997
Patent No. 5684857
GENERAL INFORMATION:
APPLICANT: SUMEDHA JAYASRNA
APPLICANT: GREG BIESECKER
APPLICANT: LARRY GOLD
APPLICANT: DREW SMITH
APPLICANT: GARY KARSCHENHEUTER
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLENDED
TITLE OF INVENTION: SELEX
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver

```

```

STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,997
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: JUNE 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: JUNE 11, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: SEPTEMBER 8, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: SEPTEMBER 17, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: FEBRUARY 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9451
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-234-997-1

Query Match 100.0% Score 45; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2,556,065;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDTF 6
Db 1 GRGDTF 6

RESULT 4
US-08-747-537-74
Sequence 74, Application US/08747137
Patent No. 5945033
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/06/747,137
2 FILING DATE: 12-MAR-1996
3 CLASSIFICATION: 424
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 06/212,546
6 FILING DATE: 14-MAR-1994
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 06/069,831
9 FILING DATE: 01-JUN-1993
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/959,560
12 FILING DATE: 13-OCT-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/641,720
15 FILING DATE: 15-JAN-1991
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Apple, Randolph T.
18 REGISTRATION NUMBER: 36,429
19 REFERENCE/DOCKET NUMBER: 016197-00,840918
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 415-576-0200
22 INFORMATION FOR SEQ ID NO: 74:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 6 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: not relevant
27 TOPOLOGY: not relevant
28 US-08-747-137-74

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Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GRGDP 6
111111
DB 1 GRGTP 6

```

```

RESULT 5
US-08-747-137-176
1 Sequence 176, Application: US/08747137
2 Patent No. 5945011
3 GENERAL INFORMATION:
4 APPLICANT: YEN, Richard C.K.
5 TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
6 THERAPEUTIC AND DIAGNOSTIC USE
7 NUMBER OF SEQUENCES: 184
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Townsend and Townsend and Crew LLP
10 STREET: Two Embarcadero Center, 8th Floor
11 CITY: San Francisco
12 STATE: CA
13 COUNTRY: USA
14 ZIP: 94111
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent's Release #1.0, Version #1.1
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/06/747,137
22 FILING DATE: 12-NOV-1996
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 06/212,546
26 FILING DATE: 14-MAR-1994
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 06/069,831
29 FILING DATE: 01-JUN-1993
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/959,560
32 FILING DATE: 13-OCT-1992
33 PRIOR APPLICATION DATA:

```

```

1 APPLICATION NUMBER: US 07/641,720
2 FILING DATE: 15-JAN-1991
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Apple, Randolph T.
5 REGISTRATION NUMBER: 36,429
6 REFERENCE/DOCKET NUMBER: 016197-000918
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 415-576-0200
9 INFORMATION FOR SEQ ID NO: 176:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 6 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: not relevant
14 TOPOLOGY: not relevant
15 US-08-747-137-176
16 Query Match 100.0%; Score 35; DB 2; Length 6;
17 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
18 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19 QY 1 GRGDP 6
20 111111
21 DB 1 GRGTP 6
22 RESULT 6
23 US-08-556-699-1
24 Sequence 1, Application: US/08956699
25 Patent No. 6085696
26 GENERAL INFORMATION:
27 APPLICANT: GREG BIESECKER
28 APPLICANT: SUMEDHA D. JAYASENA
29 APPLICANT: LARRY GOLD
30 APPLICANT: DREW SMITH
31 APPLICANT: GARY P. KIRSCHENHEUTER
32 TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
33 TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLANKET
34 NUMBER OF SEQUENCES: 5
35 CORRESPONDENCE ADDRESS:
36 ADDRESSEE: Swanson & Bratschan, L.L.C.
37 STREET: 8400 E. Prentice Avenue, Suite 100
38 CITY: Englewood
39 STATE: Colorado
40 COUNTRY: USA
41 ZIP: 80111
42 COMPUTER READABLE FORM:
43 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
44 COMPUTER: IBM PC compatible
45 OPERATING SYSTEM: MS-DOS
46 SOFTWARE: WordPerfect 6.0
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/08/556,699
49 FILING DATE: OCTOBER 23, 1997
50 CLASSIFICATION: 435
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: 08/234,997
53 FILING DATE: APRIL 28, 1994
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: 07/714,131
56 FILING DATE: JUNE 10, 1991
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: 07/536,428
59 FILING DATE: JUNE 11, 1990
60 PRIOR APPLICATION DATA:
61 APPLICATION NUMBER: 08/117,991
62 FILING DATE: SEPTEMBER 8, 1993
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: 08/123,935
65 FILING DATE: SEPTEMBER 17, 1993
66 PRIOR APPLICATION DATA:
67 APPLICATION NUMBER: 08/199,507
68 FILING DATE: FEBRUARY 22, 1994

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX15/C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3433
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-956-699-1
;
; Query Match 100.0%; Score 35; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GRGDTTP 6
; Db 1 GRGDTTP 6
;
; RESULT 7
; US-09-606-477-1
; Sequence 1, Application US/0960477
; Patent No. 6465189
; GENERAL INFORMATION:
; APPLICANT: GREG RIESECKER
; LARRY GOLD
; SUMEDHA D. CATASANA
; DREW SMITH
; GARY P. KIRSCHENHEUER
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; EXPONENTIAL ENRICHMENT: REVENUE
; SELEX
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschus, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 140
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/606,477
; FILING DATE: 29-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,699
; FILING DATE: OCTOBER 23, 1997
; APPLICATION NUMBER: 08/254,997
; FILING DATE: APRIL 28, 1994
; APPLICATION NUMBER: 07/724,133
; FILING DATE: JUNE 10, 1991
; APPLICATION NUMBER: 07/536,428
; FILING DATE: JUNE 11, 1990
; APPLICATION NUMBER: 08/117,991
; FILING DATE: SEPTEMBER 6, 1991
; APPLICATION NUMBER: 08/23,935
; FILING DATE: SEPTEMBER 17, 1993
; APPLICATION NUMBER: 08/199,507
; FILING DATE: FEBRUARY 22, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX15/C-CON

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3433
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-606-477-1
;
; Query Match 100.0%; Score 35; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GRGDTTP 6
; Db 1 GRGDTTP 6
;
; RESULT 8
; US-09-485-653-1
; Sequence 1, Application US/09485653
; Patent No. 6555321
; GENERAL INFORMATION:
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Stein, Elke
; TITLE OF INVENTION: Methods for Determining Cell Responses
; TITLE OF INVENTION: Through FcRn Receptors
; FILE REFERENCE: 22000.008501
; CURRENT APPLICATION NUMBER: US/09/485,653
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/US98/17157
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 60/056,164
; PRIOR FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: FRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 4555321e -
; OTHER INFORMATION: Synthetic construct
; US-09-485-653-1
;
; Query Match 100.0%; Score 35; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GRGDTTP 6
; Db 1 GRGDTTP 6
;
; RESULT 9
; US-09-548-697A-2
; Sequence 2, Application US/09548697A
; Patent No. 6586187
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Gopalsamy, Arinamala
; APPLICANT: Yang, Hui Y
; TITLE OF INVENTION: Methods for Solid Phase Combinatorial Synthesis of Integrin In
; FILE REFERENCE: AHP-98202
; CURRENT APPLICATION NUMBER: US/09/548,697A
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/240,952
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-548-697A-2

Query Match          100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTF 6
DB      1 GRGDTF 6

RESULT 10
PCT-US93-05640-45
; Sequence 45, Application PCT/US93/05640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millica Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610
; CLASSIFICATION:
; APPLICATION NUMBER: 07/897,983
; FILING DATE: June 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,532
; REFERENCE/DOCKET NUMBER: GC190-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-05640-45

Query Match          100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTF 6
DB      1 GRGDTF 6

RESULT 11
US-08-445-745-114
; Sequence 114, Application US/08/445745
; Patent No. 5672585
; GENERAL INFORMATION:
; APPLICANT: Pierschbacher, Michael D.
; Lukeman, David S.
; Cheng, Soan
; Craig, William S.

```

```

; APPLICANT: Pierschbacher, Michael D.
; APPLICANT: Cheng, Soan
; APPLICANT: Craig, William S.
; APPLICANT: Tschoop, Juerg F.
; TITLE OF INVENTION: Methods and Composition for Treating
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,745
; FILING DATE: 18-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,064
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/079,441
; FILING DATE: 18-JUN-1993
; APPLICATION NUMBER: US 08/050,736
; FILING DATE: 14-APR-1993
; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9825
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note="Xaa" = {Imp}"
US-08-445-745-114

Query Match          100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTF 6
DB      2 GRGDTF 7

RESULT 12
US-08-456-466-92
; Sequence 92, Application US/08/456466
; Patent No. 6395873
; GENERAL INFORMATION:
; APPLICANT: Pierschbacher, Michael D.
; Lukeman, David S.
; Cheng, Soan
; Craig, William S.

```

Tschopp, Juerg F.  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING  
THROMBOSIS

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/456,466

FILING DATE: 31-JUN-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-1A 1537

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: circular

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note- "Xaa-Pmp"

SEQUENCE DESCRIPTION: SEQ ID NO: 92:

S-08-456-466-92

Query Match 100.0%; Score 35; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GRGDIP 6

||||

D 2 GRGDIP 7

RESULT 13

S-08-445-638-114

Sequence 114, Application: US/08445638

Patent No. 6521594

GENERAL INFORMATION:

APPLICANT: Pierschbacher, Michael D.

APPLICANT: Cheng, Soan

APPLICANT: Craig, William S.

APPLICANT: Tschopp, Juerg F.

TITLE OF INVENTION: Methods and Composition for Treating

THROMBOSIS

NUMBER OF SEQUENCES: 168

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,638

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,668

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: US 08/079,411

FILING DATE: 18-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/050,736/14

FILING DATE: 14-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/681,119

FILING DATE: 05-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/506,444

FILING DATE: 06-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-1A 9829

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 114:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: circular

FEATURE:

NAME/KEY: Peptide

LOCATION: 1

OTHER INFORMATION: /note- "Xaa - {Pmp}"

US-08-445-638-114

Query Match 100.0%; Score 35; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GRGDIP 6

||||

D 2 GRGDIP 7

RESULT 14

US-08-445-745-50

Sequence 50, Application: US/08445745

Patent No. 5672585

GENERAL INFORMATION:

APPLICANT: Pierschbacher, Michael D.

APPLICANT: Cheng, Soan

APPLICANT: Craig, William S.

APPLICANT: Tschopp, Juerg F.

TITLE OF INVENTION: Methods and Composition for Treating

THROMBOSIS

NUMBER OF SEQUENCES: 168

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,745

FILING DATE:

CLASSIFICATION: 514



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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 06/171,068
3 FILING DATE: 20-DEC-1993
4 APPLICATION NUMBER: US 06/079,441
5 FILING DATE: 18-JUN-1993
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 06/050,745
8 FILING DATE: 14-APR-1993
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/681,119
11 FILING DATE: 05-APR-1991
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/506,444
14 FILING DATE: 06-APR-1990
15 APPLICATION NUMBER: US 07/506,444
16 FILING DATE: 06-APR-1990
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Campbell, Cathryn A.
19 REGISTRATION NUMBER: 31,815
20 REFERENCE/DOCKET NUMBER: P-1A 9829
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (619) 535-9061
23 TELEFAX: (619) 535-9349
24 INFORMATION FOR SEQ ID NO: 50:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 10 amino acids
27 TYPE: amino acid
28 TOPOLOGY: circular
29 FEATURE:
30 NAME/KEY: Peptide
31 LOCATION: 2
32 OTHER INFORMATION: /note: "Xaa = (Phe)"
33 US-08-445-745-50

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Query Match 100.0% Score 35: DB 17 Length 10:
Best Local Similarity 100.0% Pred. No. 0.75:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GRGDTP 6
DB 3 GRGDIP 8

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RESULT 15
US-08-445-745-51
1 Sequence 51, Application US/08445745
2 Patent No. 5672585
3 GENERAL INFORMATION:
4 APPLICANT: Pierschbacher, Michael D.
5 APPLICANT: Cheng, Sean
6 APPLICANT: Craig, William S.
7 TITLE OF INVENTION: Methods and Composition for Treating
8 TITLE OF INVENTION: Thrombosis
9 NUMBER OF SEQUENCES: 168
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Campbell and Flores
12 STREET: 4370 La Jolla Village Drive, Suite 700
13 CITY: San Diego
14 STATE: California
15 COUNTRY: USA
16 ZIP: 92122
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent In Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/445,745
24 FILING DATE:
25 CLASSIFICATION: 5.14
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 06/171,068
28 FILING DATE: 20-DEC-1993
29 APPLICATION NUMBER: US 06/079,441

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1 FILING DATE: 18-JUN-1993
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 08/050,745
4 FILING DATE: 14-APR-1993
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 07/681,119
7 FILING DATE: 05-APR-1991
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 07/506,444
10 FILING DATE: 06-APR-1990
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Campbell, Cathryn A.
13 REGISTRATION NUMBER: 31,815
14 REFERENCE/DOCKET NUMBER: P-1A 9829
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (619) 535-9061
17 TELEFAX: (619) 535-9349
18 INFORMATION FOR SEQ ID NO: 51:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 10 amino acids
21 TYPE: amino acid
22 TOPOLOGY: circular
23 FEATURE:
24 NAME/KEY: Peptide
25 LOCATION: 2
26 OTHER INFORMATION: /note: "Xaa = (Phe)"
27 US 08-445-745-51

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Query Match 100.0% Score 35: DB 17 Length 10:
Best Local Similarity 100.0% Pred. No. 0.75:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GRGDTP 6
DB 3 GRGDIP 8

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Search completed: September 16, 2003, 18:18:24
Job time : 17 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw mode:

Run on: September 16, 2003, 16:16:48 : Search time 26 seconds  
(without alignments)  
34,360 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGDP 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 556269 seqs, 148893469 residues

Total number of hits satisfying chosen parameters: 65269

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US27\_PUBCOMB.pep:
- 2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:
- 12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep:
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	12	US-10-027-270-33
2	35	100.0	6	14	US-10-027-270-33
3	35	100.0	6	15	US-10-027-270-33
4	35	100.0	1005	12	US-10-193-764-41
5	35	100.0	1005	12	US-10-193-764-41
6	32	91.4	1517	15	US-10-156-761-13265
7	31	88.6	6	9	US-09-637-969A-28
8	31	88.6	6	9	US-09-637-969A-28
9	31	88.6	6	9	US-09-637-969A-28
10	31	88.6	6	9	US-09-637-969A-28
11	31	88.6	6	10	US-09-364-597A-21
12	31	88.6	6	10	US-09-177-643-1
13	31	88.6	6	10	US-09-841-321A-26
14	31	88.6	6	10	US-09-841-321A-46
15	31	88.6	6	10	US-09-871-574-3

16	31	88.6	6	10	US-09-972-772-31	Sequence 31, Appl
17	31	88.6	6	12	US-10-262-435-5	Sequence 5, Appl
18	31	88.6	6	12	US-10-325-027-9	Sequence 9, Appl
19	31	88.6	6	14	US-10-021-943-31	Sequence 3, Appl
20	31	88.6	6	14	US-10-027-270-32	Sequence 32, Appl
21	31	88.6	6	14	US-10-027-270-35	Sequence 35, Appl
22	31	88.6	6	14	US-10-114-176-2	Sequence 2, Appl
23	31	88.6	6	15	US-10-046-801-5	Sequence 5, Appl
24	31	88.6	6	15	US-10-247-853-83	Sequence 83, Appl
25	31	88.6	6	15	US-10-138-933-4	Sequence 31, Appl
26	31	88.6	7	8	US-08-987-756-1	Sequence 1, Appl
27	31	88.6	7	10	US-05-364-597A-22	Sequence 22, Appl
28	31	88.6	7	11	US-05-911-569-8	Sequence 8, Appl
29	31	88.6	7	12	US-10-200-579-8	Sequence 8, Appl
30	31	88.6	7	12	US-10-420-029-1	Sequence 3, Appl
31	31	88.6	8	9	US-05-094-743A-96	Sequence 96, Appl
32	31	88.6	8	9	US-09-892-071-3	Sequence 3, Appl
33	31	88.6	8	10	US-05-753-126-6	Sequence 6, Appl
34	31	88.6	8	11	US-05-903-412-96	Sequence 96, Appl
35	31	88.6	8	12	US-10-165-165-96	Sequence 96, Appl
36	31	88.6	8	13	US-10-190-192-96	Sequence 96, Appl
37	31	88.6	8	15	US-10-174-717A-94	Sequence 96, Appl
38	31	88.6	9	9	US-09-492-071-11	Sequence 11, Appl
39	31	88.6	10	9	US-09-809-252-3	Sequence 1, Appl
40	31	88.6	10	9	US-09-492-071-1	Sequence 1, Appl
41	31	88.6	10	9	US-05-892-071-8	Sequence 8, Appl
42	31	88.6	10	14	US-10-007-270-32	Sequence 36, Appl
43	31	88.6	10	14	US-10-007-270-37	Sequence 37, Appl
44	31	88.6	11	9	US-09-837-969A-21	Sequence 11, Appl
45	31	88.6	11	10	US-09-841-321A-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-10-420-029-1  
Sequence 1, Application US/10420029  
Publication No. US20030157712A1  
GENERAL INFORMATION:  
APPLICANT: Daniel, Thomas C.  
APPLICANT: Stein, Elke  
TITLE OF INVENTION: Methods for Determining Cell Responses  
TITLE OF INVENTION: Through EphA Receptors  
FILE REFERENCE: 22000.008502  
CURRENT APPLICATION NUMBER: US/10/420.029  
CURRENT FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: 09/485,653  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/US98/17157  
PRIOR FILING DATE: 1998-08-19  
PRIOR APPLICATION NUMBER: 60/056,164  
PRIOR FILING DATE: 1997-08-19  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. US20030157712A1e -  
OTHER INFORMATION: Synthetic construct  
US-10-420-029-1

Query Match 100.0% Score 35: DR 12: Length 6:  
Best Local Similarity 100.0% Pred. No. 5e+05:  
Matches 6: Conservative 0: Mismatches 0: Gaps 0:

1 GRGDP 6

1 GRGDP 6

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RESULT 2
US-10-007-270-33
: Sequence 33, Application US/10-07270
: Publication No. US2002060954A1
: GENERAL INFORMATION:
: APPLICANT: Kuehn, Markus H.
: APPLICANT: Kuehn, Markus H.
: APPLICANT: University of Iowa Research Foundation
: TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
: FILE REFERENCE: 025618 000127US
: CURRENT APPLICATION NUMBER: US/10/007,270
: PRIOR FILING DATE: 2001-11-08
: PRIOR APPLICATION NUMBER: US 09/430,195
: PRIOR FILING DATE: 1999-10-29
: PRIOR APPLICATION NUMBER: US 09/183,972
: PRIOR FILING DATE: 1998-10-29
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 33
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:
: OTHER INFORMATION: RGD-containing peptide
US-10-007-270-33

Query Match          100.0%; Score 35; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6
DB 1 GRGDTTP 6

RESULT 3
US-10-263-456-1
: Sequence 1, Application US/10263456
: Publication No. US20030077646A1
: GENERAL INFORMATION:
: APPLICANT: GREG RISECKER
: APPLICANT: SUMEDIA D. JAYASENA
: APPLICANT: LARRY GOLD
: APPLICANT: DREW SMITH
: APPLICANT: GARY F. KIRSCHENHEIMER
: TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LEGAMUS HY
: TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BIENDEL
: SELEX
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESS: Swanson & Bratschus, S.L.C.
: STREET: 1745 Shea Center Drive, Suite 340
: CITY: Highlands Ranch
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80129
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
: COMPUTER: IBM pc compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 8.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/263,456
: FILING DATE: 02-Oct-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/606,477
: FILING DATE: 29-Jun-2000
: APPLICATION NUMBER: 08/956,699
: FILING DATE: OCTOBER 23, 1997
: APPLICATION NUMBER: 08/234,997
: FILING DATE: APRIL 28, 1994

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: APPLICATION NUMBER: 07/714,131
: FILING DATE: JUNE 10, 1991
: APPLICATION NUMBER: 07/536,428
: FILING DATE: JUNE 11, 1990
: APPLICATION NUMBER: 08/117,991
: FILING DATE: SEPTEMBER 6, 1994
: APPLICATION NUMBER: 08/123,935
: FILING DATE: SEPTEMBER 17, 1994
: APPLICATION NUMBER: 08/199,507
: FILING DATE: FEBRUARY 22, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEXIS/C-CAN
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-263-456-1

Query Match          100.0%; Score 35; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6
DB 1 GRGDTTP 6

RESULT 4
US-10-193-764-41
: Sequence 41, Application US/10193764
: Publication No. US20030133943A1
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena M.
: APPLICANT: Yang, Yan-Ping
: APPLICANT: Klein, Michel H.
: TITLE OF INVENTION: PROTECTIVE PEPTOMINANT HAEMOPHILUS INFLUENZAE HIGH
: TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
: FILE REFERENCE: 1038-1239MIS
: CURRENT APPLICATION NUMBER: US/10/193,764
: CURRENT FILING DATE: 2002-07-12
: PRIOR APPLICATION NUMBER: 09/167,568
: PRIOR FILING DATE: 1998-10-07
: NUMBER OF SEQ ID NOS: 91
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 41
: LENGTH: 1005
: TYPE: PRT
: ORGANISM: Haemophilus influenzae
US-10-193-764-41

Query Match          100.0%; Score 35; DB 12; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6
DB 19 GRGDTTP 24

RESULT 5
US-10-193-764-39
: Sequence 39, Application US/10193764
: Publication No. US20030133943A1
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena M.

```

; APPLICANT: Yang, Yan-Ping  
 ; APPLICANT: Klein, Michel B.  
 ; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH  
 ; TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS  
 ; FILE REFERENCE: 1038-1239MIS  
 ; CURRENT APPLICATION NUMBER: US/10/295,764  
 ; PRIOR FILING DATE: 2002-07-12  
 ; PRIOR APPLICATION NUMBER: 09/167,566  
 ; PRIOR FILING DATE: 1998-10-07  
 ; NUMBER OF SEQ ID NOS: 91  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 39  
 ; LENGTH: 1011  
 ; TYPE: PRT  
 ; ORGANISM: Haemophilus influenzae  
 US-10-193-764-39

Query Match 100.0% Score 32; DB 12; Length 1011  
 Best Local Similarity 100.0%; Pred. No. 7.6e-02  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 11111  
 DB 25 GRGDTP 30

## RESULT 6

US-10-156-761-13265  
 ; Sequence 13265, Application US/0156761  
 ; Publication No. US20030119018A1

; GENERAL INFORMATION:  
 ; APPLICANT: OMURA, SATOSH;  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIDA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; APPLICANT: HATTORI, MASAHARA  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-262  
 ; CURRENT APPLICATION NUMBER: US/10/156,761  
 ; CURRENT FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2001-204089  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2001-272697  
 ; PRIOR FILING DATE: 2001-09-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 13265  
 ; LENGTH: 1517  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis

US-10-156-761-13265

Query Match 91.4% Score 32; DB 15; Length 1517  
 Best Local Similarity 83.3%; Pred. No. 7.6e-02  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 11111  
 DB 1512 GRGDTP 1517

## RESULT 7

US-09-837-969A-28  
 ; Sequence 28, Application US/09837969A  
 ; Patent No. US20020030150A1

; GENERAL INFORMATION:  
 ; APPLICANT: Uryu, Dan  
 ; TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
 ; FILE REFERENCE: BERL-020/030S  
 ; CURRENT APPLICATION NUMBER: US/09/837,969A  
 ; CURRENT FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 09/258,723

; PRIOR FILING DATE: 1999-02-26  
 ; PRIOR APPLICATION NUMBER: US 60/087155  
 ; PRIOR FILING DATE: 1998-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/076297  
 ; PRIOR FILING DATE: 1998-02-27  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 28  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(6)  
 ; OTHER INFORMATION: Synthetic  
 US-09-837-969A-28

Query Match 88.6% Score 31; DB 9; Length 6  
 Best Local Similarity 83.3%; Pred. No. 5e+05  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 11111  
 DB 1 GRGDTP 6

## RESULT 8

US-09-837-969A-46  
 ; Sequence 46, Application US/09837969A  
 ; Patent No. US20020030150A1

; GENERAL INFORMATION:  
 ; APPLICANT: Uryu, Dan  
 ; TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
 ; FILE REFERENCE: BERL-020/030S  
 ; CURRENT APPLICATION NUMBER: US/09/837,969A  
 ; CURRENT FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 09/258,723  
 ; PRIOR FILING DATE: 1999-02-26  
 ; PRIOR APPLICATION NUMBER: US 60/067155  
 ; PRIOR FILING DATE: 1998-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/076297  
 ; PRIOR FILING DATE: 1998-02-27  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 46  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(6)  
 ; OTHER INFORMATION: Synthetic  
 US-09-837-969A-46

Query Match 88.6% Score 31; DB 9; Length 6  
 Best Local Similarity 83.3%; Pred. No. 5e+05  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 11111  
 DB 1 GRGDTP 6

## RESULT 9

US-09-888-260-15  
 ; Sequence 15, Application US/09888260  
 ; Patent No. US20020068304A1

; GENERAL INFORMATION:  
 ; APPLICANT: Bioelastics Research, Ltd.  
 ; APPLICANT: Uryu, Dan  
 ; TITLE OF INVENTION: Bioelastomer Nanomachines and Biosensors  
 ; FILE REFERENCE: BERL-030/010S  
 ; CURRENT APPLICATION NUMBER: US/09/888,260

```

: CURRENT FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: 60/213,344
: PRIOR FILING DATE: 2003-06-23
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn version 1.0
: SEQ ID NO 15
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: PETIDE
: LOCATION: (1)..(6)
: OTHER INFORMATION: Synthetic
US-09-888-260-15

Query Match      88.6%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. Hits: 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTF 6
Db      1 GRGDSP 6
      111111

RESULT 10
US-09-961-834-1
: Sequence 1, Application US/9961834
: Patent No. US20020081726A;
: GENERAL INFORMATION:
: APPLICANT: Russell et al.
: TITLE OF INVENTION: MICROFABRICATION OF MEMBRANES FOR THE GROWTH OF CELLS
: FILE REFERENCE: 27611/37761
: CURRENT APPLICATION NUMBER: US/09/961,834
: CURRENT FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: US 60/235,094
: PRIOR FILING DATE: 2000-09-25
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Fibronectin ligand receptor
US-09-961-834-1

Query Match      89.6%; Score 41; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. Hits: 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTF 6
Db      1 GRGDSP 6
      111111

RESULT 11
US-09-364-597A-21
: Sequence 21, Application US/99364597A
: Patent No. US2002010330A1
: GENERAL INFORMATION:
: APPLICANT: Roosthali, Ekki
: APPLICANT: Roosthali, Ekki
: TITLE OF INVENTION: NO. US2002010330A1; INTEGRIN-BINDING PEPTIDES
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLC
: STREET: 4370 La Jolla Village Drive, Suite 702
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/364,597A
: FILING DATE: 30-JUL-1999
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 68/156,601
: FILING DATE: 24-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 68/285,861
: FILING DATE: 04-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-JA 3419
: TELEPHONE: (858) 535-9001
: TELEFAX: (858) 535-8949
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-09-364-597A-21

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. Hits: 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTF 6
Db      1 GRGDSP 6
      111111

RESULT 12
US-09-177-843-1
: Sequence 1, Application US/09177843
: Patent No. US20020114804A1
: GENERAL INFORMATION:
: APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE
: APPLICANT: CITY OF NEW YORK
: TITLE OF INVENTION: A METHOD OF PREVENTING AND TREATING
: TITLE OF INVENTION: BACTERIAL INFECTION OF SUTURES AND
: TITLE OF INVENTION: PROSTHETIC DEVICES, AND PROMOTING
: TITLE OF INVENTION: INGRESS OF LEUKOCYTES INTO TUMOR
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/177,843
: FILING DATE: April 22, 1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 48940-A-PCT/JPW/CKM
: TELEPHONE: 212-278-0400
: TELEFAX: 212-391-0525
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids

```

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-177-843-1

```

```

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GRGDTP 6
   |||||
DB 1 GRGDSP 6

```

## RESULT 13

```

US-09-841-321A-28
; Sequence 28, Application US/09841321A
; Patent No. US20020116059A1
; GENERAL INFORMATION:
; APPLICANT: Urvy, Dan
; TITLE OF INVENTION: Injectable Implants for Tissue Augmentation and Restoration
; FILE REFERENCE: BERL-020/0405
; CURRENT APPLICATION NUMBER: US/09/841-321A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/258,723
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 60/087155
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: US 60/076297
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(6)
; OTHER INFORMATION: Synthetic
US-09-841-321A-28

```

```

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GRGDTP 6
   |||||
DB 1 GRGDSP 6

```

## RESULT 14

```

US-09-841-321A-46
; Sequence 46, Application US/09841321A
; Patent No. US20020116059A1
; GENERAL INFORMATION:
; APPLICANT: Urvy, Dan
; TITLE OF INVENTION: Injectable Implants for Tissue Augmentation and Restoration
; FILE REFERENCE: BERL-020/0405
; CURRENT APPLICATION NUMBER: US/09/841-321A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/258,723
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 60/087155
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: US 60/076297
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46

```

```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(6)
; OTHER INFORMATION: Synthetic
US-09-841-321A-46

```

```

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GRGDTP 6
   |||||
DB 1 GRGDSP 6

```

## RESULT 15

```

US-09-871-974-3
; Sequence 3, Application US/09871974
; Patent No. US20020147136A1
; GENERAL INFORMATION:
; APPLICANT: VON WRONSKI, MATHEW A.
; APPLICANT: MARINELLI, EDMOND R.
; APPLICANT: NUNN, ADRIAN D.
; APPLICANT: PILLAI, RADHAKRISHNA
; APPLICANT: RAMALINGAM, KONDAREDDI, AR
; APPLICANT: TWEDDE, MICHAEL F.
; APPLICANT: LINDER, KAREN
; APPLICANT: NANJAPPAN, PALANIAPPA
; APPLICANT: RAJU, NATARAJAN
; TITLE OF INVENTION: COMPOUNDS FOR TARGETING ENDOCELLULAR CELLS, COMPOSITIONS
; FILE REFERENCE: 2238-7
; CURRENT APPLICATION NUMBER: US/09/871,974
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 09/585,364
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-871-974-3

```

```

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GRGDTP 6
   |||||
DB 1 GRGDSP 6

```

```

Search completed: September 16, 2003, 15:18:56
Job time : 27 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Inc.

OM protein - protein search, using sw model

Run On: September 16, 2003, 14:15:07 / Search time 15 Seconds  
(without alignments)  
34,462 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGDTP 6

Scoring table: HUSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616662 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 3

Maximum DB seq length: 2500000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_761

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	370	2 S27344	luck protein - Rhi
2	35	100.0	450	2 D87342	multidrug resist
3	35	100.0	1307	2 T40867	246D nuclear prote
4	32	91.4	266	1 S8159	ribosomal protein
5	32	91.4	458	2 T22571	probable myosin
6	32	91.4	606	2 AC2508	hypothetical prote
7	32	91.4	1226	2 S44824	F54F2.2 protein
8	31	88.6	273	2 A28512	fibronectin - chis
9	31	88.6	359	2 S84270	hypothetical prote
10	31	88.6	425	1 S88469	probable membrane
11	31	88.6	438	2 B82042	osmolarity sensor
12	31	88.6	441	2 S74264	isocitrate synt
13	31	88.6	463	1 S74845	14D homolog sir08
14	31	88.6	515	2 A39675	probable oxidore
15	31	88.6	515	2 D95525	probable oxidore
16	31	88.6	606	2 T23100	hypothetical prote
17	31	88.6	691	2 T45333	hypothetical prote
18	31	88.6	1020	2 A29385	fibronectin - chis
19	31	88.6	2265	1 FNRO	fibronectin - rev
20	31	88.6	2386	1 FNRC	fibronectin precu
21	31	88.6	2477	2 S14434	fibronectin - ARI
22	31	88.6	2481	2 A43928	fibronectin - ARI
23	30	85.7	253	2 S84258	hypothetical prote
24	30	85.7	277	2 A83256	aminoglycoside
25	30	85.7	299	2 C55213	rbc protein - Shi
26	30	85.7	317	2 A75477	cysteine synthase
27	30	85.7	335	1 KPR08	cathepsin B (EC 3.
28	30	85.7	339	1 KHR08	cathepsin B (EC 3.
29	30	85.7	339	1 KHR08	cathepsin B (EC 3.

ALIGNMENTS

RESULT 1  
S27344

hpx protein - Rhizobium leguminosarum

C:Species: Rhizobium leguminosarum

C:Date: 25-Oct-1994 #sequence\_revision 01-Dm-1995 #text\_change 08-Oct-1999

C:Accession: S27344

R:Ref: L. Hidalgo, E. Palacios, J. Ruiz-Arguieso, E.

C. Mol. Biol. 228, 998-1002, 1992

A:Title: Nucleotide sequence and organization of an R(2) uptake gene cluster from Rhi

A:Reference number: S27340; X010:93108466; PMID:1459753

A:Accession: S27344

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-370 <RAY>

A:Cross-references: EMBL:X52974; NID:q167855; PIRN:CAA97156.1; PIR:q48731

Query Match 100.0% Score 35; DB 2; Length 370;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6

DB 163 GRGDTP 168

RESULT 2  
D87342

multidrug resistance protein, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: D87342

K.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.I.; Nelson, K.E.; Eisen, J.; Heidelberg,

n. J.; Laub, M.T.; Deboy, K.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.L.; K

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; X010:2117698; PMID:11259667

A:Accession: D87342

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-450 <STO>

A:Cross-references: GB:AE005673; NID:g13421986; PIRN:AAK22736.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0751

Query Match 100.0% Score 35; DB 2; Length 450;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6

DB 220 GRGDTP 225

RESULT 3  
 T30887  
 146D nuclear protein - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jul-2000  
 C:Accession: T30887  
 R:Schmidt-Zachmann, M.S.; Knecht, S.; Kraemer, A.  
 Mol. Biol. Cell 9, 143-160, 1998  
 A:Title: Molecular characterization of a novel, widespread nuclear protein that colocalizes with the nucleolus in *Xenopus laevis*  
 A:Reference number: 420921; MID:94093695; PMID:9445997  
 A:Accession: T30887  
 A:Status: preliminary; translated from GH/EMBL/PCRJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1307 <SCH>  
 A:Cross-references: EMBL:Y08997; NID:92791835; PDB:CAA70201.1; PDB:2731896  
 Query Match 100.0%; Score 35; DB 2; Length 1307  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 1 GRGDTP 6  
 DB 272 GRGDTP 277  
 RESULT 4  
 S18159  
 Ribosomal protein L7a, cytosolic - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 22-Jun-1999  
 C:Accession: A46032; F50415; S18159  
 R:Colombo, P.; Yon, J.; Garson, K.; Fried, M.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 6369-6372, 1993  
 A:Title: Conservation of the organization of five tightly clustered genes over 600 million years  
 A:Reference number: A46032; MIM:62335297; PMID:1631131  
 A:Accession: A46032  
 A:Molecule type: mRNA; DNA  
 A:Residues: 1-266 <COL>  
 A:Cross-references: EMBL:X62640; NID:953777; PDB:CAA44505.1; PDB:563778  
 A:Note: submitted to the EMBL Data Library, October 1991  
 A:Note: sequence extracted from NCBI backbone (NCBI:P108743)  
 R:Maeda, N.; Kenmochi, N.; Tanaka, T.  
 Biochimie 75, 785-790, 1993  
 A:Title: The complete nucleotide sequence of chicken ribosomal protein L7a gene and the cDNA  
 A:Reference number: F50416; MIM:64162270; PMID:8274596  
 A:Accession: F50416  
 A:Status: translated from GH/EMBL/PCRJ  
 A:Molecule type: rRNA  
 A:Residues: 1-266 <MAE>  
 A:Cross-references: GH:P144522; NID:9457652; PDB:MAA0095.1; PDB:9400344  
 C:Genetics:  
 A:Gene: surr-3/Rp.7a  
 A:Introns: 1/3; 42/1; 92/1; 135/1; 165/1; 259/2; 282/3  
 C:Superfamily: rat ribosomal protein L7a  
 C:Keywords: protein biosynthesis; ribosome  
 Query Match 91.4%; Score 32; DB 1; Length 266  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0  
 QY 1 GRGDTP 6  
 DB 124 GRGDTP 129  
 RESULT 5  
 T02571  
 Probable myosinase-binding protein [imported] - Arabidopsis thaliana  
 A:Alternate names: hypothetical protein T16824.5  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001

C:Accession: T02571; G84815  
 R:Mounslow, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke  
 submitted to the EMBL Data Library, August 1998  
 A:Description: Arabidopsis thaliana chromosome II PAC T16824 genomic sequence.  
 A:Reference number: 214679  
 A:Accession: T02571  
 A:Status: translated from GS/EMBL/PCRJ  
 A:Molecule type: DNA  
 A:Residues: 1-458 <ROD>  
 A:Cross-references: EMBL:AC004697; NID:93462671; PDB:93402675  
 A:Experimental source: Cultivar Colombia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shree, J.P.; Ruito, M.L.; Town, C.D.; Fujii, C.Y.  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VarAken, S.E.; Umayam, L.; Telson,  
 G.S.; D.; Nicmar, W.C.; White, G.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
 Nature 402, 763-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MIM:62083487; PMID:10617197  
 A:Accession: G84815  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-458 <STO>  
 A:Cross-references: GB:AE002093; NID:93402676; PDB:AA023979.1; GSPEB:GN00139  
 C:Genetics:  
 A:Gene: T16824.5; At2g39310  
 A:Map position: 2  
 A:Introns: 67/3; 221/3; 374/3  
 Query Match 91.4%; Score 32; DB 2; Length 458  
 Best Local Similarity 83.3%; Pred. No. 97;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0  
 QY 1 GRGDTP 6  
 DB 214 GRGDTP 219  
 RESULT 6  
 AC2508  
 hypothetical protein alr7243 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC712  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C:Accession: AC2508  
 R:Kakazu, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Susamoto, S.; Watanabe, A.; Iriku  
 Kakazu, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium  
 A:Reference number: AB1807; MIM:21595235; PMID:11759840  
 A:Accession: AC2508  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-606 <KUR>  
 A:Cross-references: GB:BA000320; PDB:HAB78327.1; PDB:17195781; GSPEB:GN00180  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr7243  
 A:Genome: plasmid  
 Query Match 91.4%; Score 32; DB 2; Length 606  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0  
 QY 1 GRGDTP 6  
 DB 120 GRGDTP 125  
 RESULT 7  
 S44824  
 P54f2.1 protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001  
 C:Accession: S44824



R:Anderson, K.  
 submitted to the EMBL Data Library, September 1993  
 A:Description: Sequence of the *C. elegans* cosmid F54F2.  
 A:Reference number: S448.7  
 A:Accession: S44824  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1226 <ANI>  
 A:Cross-references: EMBL:L23645; NID:q388603; PID:q388605  
 C:Genetics:  
 A:Introns: 58/2; 137/3; 179/2; 316/2; 393/1; 552/3; 597/2; 662/2; 855/3; 1178/4  
 C:Keywords: cytoskeleton; transmembrane protein

Query Match 81.48; Score 52; DP 2; Length 1226;  
 Best Local Similarity 83.38; Pred. No. 53;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 III:II

DB 519 GRGDTP 524

RESULT 8  
 A28512  
 fibronectin - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 31-Dec-1988 #sequence\_revision 1; text\_change 20-Aug-1993  
 C:Accession: A28512  
 R:Kubomura, S.; Gbara, M.; Karsenti, Y.; Tachibana, H.; Goto, S.; Tsutsi, T.; Hiroshi, K.  
 Biochim. Biophys. Acta 913; 171-181; 1987  
 A:Title: Genetic analysis of the cell binding domain region of the chicken fibronectin  
 A:Reference number: A28512; MIM:28050550; PMID:2823899  
 A:Accession: A28512  
 A:Molecule type: DNA  
 A:Residues: 1-273 <KOR>  
 A:Cross-references: GB:X06533; NID:q363993; PID:CAA9761.1; PID:q297716  
 A:Note: The authors translated the codon CCG for residue 190 as Gln, CAG for residue 243  
 C:Genetics:  
 A:Introns: 90/1; 123/1; 184/1; 236/1  
 C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat  
 C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter  
 F:1-82/Domain: fibronectin type III repeat homology (fragment) <EN31>  
 F:90-172/Domain: fibronectin type III repeat homology <EN33>  
 F:167-169/Region: cell attachment (R-G-D) motif  
 F:184-265/Domain: fibronectin type III repeat homology <EN35>

Query Match 89.68; Score 31; DP 2; Length 273;  
 Best Local Similarity 83.38; Pred. No. 53;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 III:II

DB 166 GRGDSP 171

RESULT 9  
 G84270  
 hypothetical protein Vng1149c [imported] - Halobacterium sp. NRC-1  
 C:Species: Halobacterium sp. NRC-1  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: G84270  
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, S.G.; Berquist, B.; Paz, M.; Shukla, H.; Lasky, S.  
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, J.D.; Jablo  
 Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97; 12176-12181; 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, F.P.; Greer, A.D.; Elhardt, H.; Lowe, T.M.; Li  
 A:Title: Genome sequence of Halobacterium species NRC-1.  
 A:Reference number: A84160; MIM:20504461; PMID:11016950  
 A:Accession: G84270  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-399 <STO>  
 A:Cross-references: GB:AE004437; NID:gl0580687; PID:AA01531.1; GSPB:GN00138

## C:Genetics:

A:Gene: VNG1149C

Query Match 88.68; Score 31; DP 2; Length 399;  
 Best Local Similarity 83.38; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 III:II

DB 287 GRGETP 292

## RESULT 10

S48459

probable membrane protein YII133w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Apr-2002

C:Accession: S48459

R:Howman, S.; Churcher, C.

submitted to the EMBL Data Library, September 1994

A:Reference number: S48455

A:Accession: S48459

A:Molecule type: DNA

A:Residues: 1-425 &lt;BOV&gt;

A:Cross-references: GB:Z47047; EMBL:Z48125; NID:q761243; GSPB:GN03009;

## C:Genetics:

A:Gene: MIP5; YII133w

A:Cross-references: SGD:SC0001455

A:Map position: 9L

C:Superfamily: Archaeoglobus fulgidis conserved hypothetical protein AF1803

C:Keywords: transmembrane protein

F:155-177/Domain: transmembrane #status predicted &lt;TM&gt;

F:334-350/Domain: transmembrane #status predicted &lt;TM&gt;

Query Match 86.68; Score 31; DP 1; Length 425;  
 Best Local Similarity 83.38; Pred. No. 85;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 III:II

DB 415 GRGETP 420

## RESULT 11

S82042

osmolarity sensor protein EnvZ VC2713 [imported] - Vibrio cholerae (strain N1695; se

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: S82042

R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Swinn, M.L.; Dodson, R

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Saller

; R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406; 477-483; 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MIM:20466833; PMID:10952401

A:Accession: S82042

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-438 &lt;HKL&gt;

A:Cross-references: GB:AE004337; GB:AE003352; NID:q9457307; PID:AA958553.1; GSPB:G

A:Experimental source: serogroup O1; strain N1695; biotype F1 Tor

## C:Genetics:

A:Gene: VC2713

A:Map position: 1

Query Match 88.68; Score 31; DP 2; Length 438;  
 Best Local Similarity 83.38; Pred. No. 88;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 III:II

DB 190 GRGETP 195

```

RESULT 12
E84264
isochorismate synthase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84264
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.B.; Perquist, H.J.; Fan, M.; Soule, H.D.; Caskey, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hord, D.W.; Madhock, D.G.; Jaffe
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hord, S.; Daniels, C.J.; Dennis, P.F.; Ozeri, A.D.; Eshard, H.; Lowe, T.M.; Le
A:Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; M010:20504483; PMID:11316952
A:Accession: E84264
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <STO>
A:Cross-references: GB:AE004437; NID:91058369; P11N:AA019411; GSPDB:GN00138
C:Genetics:
A:Gene: menF

Query Match 86.6%; Score 31; DB 2; Length 441;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6
DB 271 GRGDSF 276
|||||

RESULT 13
S74845
tldD homolog slr0863 - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 16-Jun-2006
C:Accession: S74845
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watarabe, A.; Yamada, N.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.
A:Reference number: S74322; M010:97051201; PMID:8905241
A:Accession: S74845
A:Molecule type: DNA
A:Residues: 1-463 <KAN>
A:Cross-references: EMBL:U09090; GB:AH001349; NID:91558441; P11N:BA012906; F01094:65248
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Escherichia coli tldD protein

Query Match 88.6%; Score 31; DB 1; Length 463;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6
DB 352 GRGTFP 357
|||||

RESULT 14
A99675
probable oxidoreductase subunit E850369 [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A99675
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishio, K.; Yokoyama, K.; Kan, C.G.;
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; M010:21156231; PMID:11258796
A:Accession: A99675
A:Status: preliminary

```

```

A:Molecule type: DNA
A:Residues: 1-515 <HAY>
A:Cross-references: GB:BA003007; P11N:BA033792.1; F01094:559926; GSPDB:GN00154
A:Experimental source: strain O157:H7, Substrain KMD 350992
C:Genetics:
A:Gene: E850369

Query Match 88.6%; Score 31; DB 2; Length 515;
Best Local Similarity 83.3%; Pred. No. 14402;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6
DB 284 GRGTFP 289
|||||

RESULT 15
B85525
probable oxidoreductase subunit yahF [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85525
R:Perica, N.L.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
ilicz, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Damalanta, E.; Potamoudis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; M010:21074535; PMID:11206551
A:Accession: B85525
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <STO>
A:Cross-references: GB:AE005174; NID:91253137; P11N:AA054664.1; GSPDB:GN00145; JWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yahF

Query Match 88.6%; Score 31; DB 2; Length 515;
Best Local Similarity 83.3%; Pred. No. 16402;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6
DB 284 GRGTFP 289
|||||

Search completed: September 16, 2003, 18:11:01
Job time : 16 secs

```

GenCorp version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:15:27 : Search time 12 seconds  
(without alignments)  
23,523 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GSKDTP 5

Scoring table: BLOSUM62

Gapop 17.0 , Gapext 0.5

Searched: 127863 seqs, 47626765 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 04

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Description	ID
1	35	100.0	HUPK_RHLIV	P29153 Rhizobium l
2	35	100.0	S381_HUMAN	O75533 homo sapien
3	35	100.0	S381_MOUSE	O99809 mus musculu
4	35	100.0	S381_XENLA	O57683 xenopus lae
5	32	91.4	R17A_CHICK	P34229 gallus gall
6	32	91.4	MB22_ARATH	O80950 arabidopsis
7	32	91.4	PA72_CAEEL	P34446 caeciliadidi
8	31	88.6	Y1K3_YEAST	P46487 saccharomyc
9	31	88.6	Y863_SYNY3	P71754 synergomyc
10	31	88.6	FINC_CHICK	P11722 gallus gall
11	31	88.6	FINC_FLEWA	Q91269 p.aurodules
12	31	88.6	FINC_BOVIN	P07559 bos taurus
13	31	88.6	FINC_HUMAN	P02751 homo sapien
14	31	88.6	FINC_MOUSE	P11276 mus musculu
15	31	88.6	FINC_RAT	P04937 rattus norv
16	31	88.6	FINC_XENLA	Q91240 xenopus lae
17	30	85.7	G332_HALNI	Q99859 halobacteri
18	30	85.7	RFBD_STRFL	P37778 shigella fl
19	30	85.7	CATR_BOVIN	P07698 bos taurus
20	30	85.7	CATR_HUMAN	P07558 homo sapien
21	30	85.7	CATR_MOUSE	P10605 mus musculu
22	30	85.7	CATR_RAT	P04787 rattus norv
23	30	85.7	ACR3_RAT	P04757 rattus norv
24	30	85.7	NAB2_STRCO	Q5X808 streptomyc
25	30	85.7	H570_DAJCA	P26791 daucus caro
26	30	85.7	SM6A_HUMAN	Q45266 homo sapien
27	29	82.9	R1S9_MYCLE	Q98604 mycobacteri
28	29	82.9	KSER_FOELI	P38136 escherichia
29	29	82.9	NHAB_RHOS	Q51117 rhodococcus
30	29	82.9	CRTA_RHICA	P17055 rhodobacter
31	29	82.9	R278_YEAST	P21771 saccharomyc
32	29	82.9	POA_SMSAV	P03359 simian sarc
33	29	82.9	ACCA_ALCEU	P27745 alcaligenes

34	29	82.9	343	1	GAS1_MOUSE	Q01721 mus musculu
35	29	82.9	345	1	GAS1_HUMAN	P54826 homo sapien
36	29	82.9	367	1	RECF_CAUCK	P49998 caulobacter
37	29	82.9	425	1	POH1_BRARE	P31366 brachydanio
38	29	82.9	432	1	LMB1_VIBPA	P59494 vibrio para
39	29	82.9	436	1	IBX6_HUMAN	O95947 homo sapien
40	29	82.9	443	1	2P23_BRARE	P79745 brachydanio
41	29	82.9	467	1	VE2_HPV24	P50770 human papil
42	29	82.9	493	1	CPE1_HUMAN	P51581 homo sapien
43	29	82.9	493	1	CPE1_MESAU	P51581 mesocricetu
44	29	82.9	493	1	CPE1_MOUSE	Q05421 mus musculu
45	29	82.9	493	1	CPE1_RAT	P05182 rattus norv

## ALIGNMENTS

RESULT 1						
HUPK_RHLIV						
ED	HUPK_RHLIV	STANDARD:	FRG:	370	AA:	
AC	P29153:					
OT	01-JUL-1993 (Rel. 26, Created)					
OT	01-FEB-1996 (Rel. 33, Last sequence update)					
ET	30-MAY-2000 (Rel. 39, Last annotation update)					
DE	Hydrogenase expression/formation protein hupK.					
QM	HUPK.					
OS	Rhizobium leguminosarum (biovar viciae).					
GT	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;					
OP	Rhizobiaceae; Rhizobium/Azorhacterium group; Rhizobium					
OX	NCBI_TaxID:387;					
EN	[[					
SC	SEQUENCE FROM N.A.					
RC	STRAIN:J28C53;					
EX	MEDLINE:93108466; PubMed:1469733;					
RA	Key L., Hidalgo E., Palacios J.M., Ruiz-Arqueso T.J.					
RT	"Nucleotide sequence and organization of an h2 uptake gene cluster					
RT	from Rhizobium leguminosarum bv. viciae containing a h2rdoxin-like					
RT	gene and four additional open reading frames.";					
RC	J. Mol. Biol. 228:998-1002(1992).					
SK	2).					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE:95020662; PubMed:7934943;					
RA	Imperial J., Rey L., Ruiz-Arqueso T.J.					
RT	"HupK, a hydrogenase-ancillary protein from Rhizobium leguminosarum,					
RT	shares structural motifs with the large subunit of Nite hydrogenases					
RT	and could be a scaffolding protein for hydrogenase metal cofactor					
RT	assembly.";					
RL	Mol. Microbiol. 9:1305-1306(1993).					
RN	3).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-B10;					
RA	Rito B., Palacios J.M., Imperial J., Ruiz-Arqueso T., Yang W.C.,					
RA	Bissegling T., Schmitt H., Keri V., Bauer T., Kokorek W., Lotz W.,					
RT	"Organization of the hup-region and its differential transcription					
RT	in non-symbiotic and symbiotic cells of Rhizobium leguminosarum					
RT	bv. viciae B10.";					
RL	Mol. Plant Microbe Interact. 8:235-240(1997).					
CC	-1. SIMILARITY: BELONGS TO THE HUPK FAMILY.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC	-----					
CC	EMBL: X52974; CAA37158.1;					
DR	EMBL: Z36981; CAA85440.1;					
DR	PIR: S27344; S27344.					
FT	CONFICT 240 240					
FT	SEQUENCE 370 AA: 38751 MW: ED17BC76B52F28C9 CRO64;					
FT	A -> R (N REF. 1).					

Query Match 100.0% Score 35: DB 1: Length 370;  
 Best Local Similarity 100.0% Pred. No. 3.2;  
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 GRGDP 6  
 DB 161 GRGDP 168

RESULT 2  
 S3B1\_HUMAN STANDARD: PRT: 1304 AA.  
 AC Q75533;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3B155) (Pre-mRNA splicing factor SF3B 155 kDa subunit).  
 GN SF3B1 OR SAPI55.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION.  
 RX MEDLINE=9825826; PubMed=9585501;  
 RA Wang C., Chua K., Sequenzi W., Lees E., Gozani O., Reed R.;  
 RT "phosphorylation of spliceosomal protein SAP 155 coupled with splicing catalysis".;  
 RL Genes Dev. 12:1409-1414(1998).  
 RN [2]  
 RP SEQUENCE OF 1011-1304 FROM N.A.  
 RC TISSUE=Brain;  
 RA Yu W., Gibbs R.A.;  
 RN [3]  
 RP Submitted (JUN-1998) to the EMBL/GenBank/CCBJ databases.  
 RN [4]  
 RP CHARACTERIZATION OF THE SPLICEDOME.  
 RX MEDLINE=20337962; PubMed=10862114;  
 RA Das R., Zhou Z., Reed R.;  
 RT "Functional association of U2 snRNP with the ATP-independent spliceosomal complex E".;  
 RL Mol. Cell 5:779-787(2000).  
 CC -!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR 'A' COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (HPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX. BELONGS ALSO TO THE MINOR U12-DEPENDENT SPLICEDOME, WHICH IS INVOLVED IN THE SPLICING OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON.  
 CC -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED OF FOUR SUBUNITS: SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145, AND A SF3B1/SAP155. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP). SF3B1 INTERACTS DIRECTLY WITH THE SPLICING FACTOR U2AF (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- PTM: PHOSPHORYLATED. PHOSPHORYLATION OCCURS CONCOMITANT WITH THE CATALYTIC STEPS OF SPLICING.  
 CC -!- SIMILARITY: BELONGS TO THE SF3B1 FAMILY.  
 CC -!- SIMILARITY: Contains 2 HEAT repeats.  
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 CC -----  
 CC EMBL: AF054284; AAC97189.1;  
 CC EMBL: AF070540; AAC28633.1;  
 CC DR

DR Genex: HGNC:10768; SF3B1.  
 DR CK: Q75533;  
 DR MM: 605590;  
 DR CC: GO:0005681; C:spliceosome complex; NAS.  
 DR CC: GO:0008248; P:pre-mRNA splicing factor activity; NAS.  
 DR CC: GO:0006371; P:mRNA splicing; NAS.  
 DR CC: GO:0006371; P:mRNA splicing; NAS.  
 KW Spliceosome: mRNA processing; mRNA splicing; Nuclear protein;  
 KW phosphorylation; Repeat;  
 SO SEQUENCE 1304 AA; 145814 MR; 40DB21A62691E5A7 CDS64;

Query Match 100.0% Score 35: DB 1: Length 3104;  
 Best Local Similarity 100.0% Pred. No. 13;  
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 GRGDP 6  
 DB 269 GRGDP 274

RESULT 3  
 S3B1\_MOUSE STANDARD: PRT: 1304 AA.  
 ID S3B1\_MOUSE  
 AC Q99NB9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3B155) (Pre-mRNA splicing factor SF3B 155 kDa subunit).  
 GN SF3B1 OR SAPI55.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus;  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=21189985; PubMed=11252167;  
 RA Isono K., Abe K., Tomari Y., Okazaki Y., Hayashizaki Y., Koseki H.;  
 RT "Molecular cloning, genetic mapping, and expression of the mouse Sf3b1 (SAP155) gene for the U2snRNP component of spliceosome".;  
 RL Mamm. Genome 12:192-198(2001).  
 CC -!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR 'A' COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (HPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX. BELONGS ALSO TO THE MINOR U12-DEPENDENT SPLICEDOME, WHICH IS INVOLVED IN THE SPLICING OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON (BY SIMILARITY).  
 CC -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED OF FOUR SUBUNITS: SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145, AND A SF3B1/SAP155. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP). SF3B1 INTERACTS DIRECTLY WITH THE SPLICING FACTOR U2AF (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- PTM: PHOSPHORYLATED. PHOSPHORYLATION OCCURS CONCOMITANT WITH THE CATALYTIC STEPS OF SPLICING (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE SF3B1 FAMILY.  
 CC -!- SIMILARITY: Contains 2 HEAT repeats.  
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 CC -----  
 CC EMBL: AB037890; BAB40140.1;  
 CC EMBL: MGI:1932339; Sf3b1.  
 CC DR

DR EMBL: AF070540; AAC28633.1;  
 KW Spliceosome: mRNA processing; mRNA splicing; Nuclear protein.

KW Phosphorylation; Repeat.  
SQ SEQUENCE 1304 AA; 145816 MW; 12F0521757D2A2DEE CRC64;

Query Match 100.0%; Score 35; DB 1; Length 1304;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
|||||  
DB 269 GRGDP 274

RESULT 4  
S3BL\_XENIA STANDARD; PRT: 1307 AA.

ID S3BL\_XENIA  
AC 057633;  
DT 16-OCT-2001 (Rel. 40, Created)  
DI 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP155) (S3BL155) (Pre-mRNA splicing factor SF3B155 kDa subunit) [14]  
DE kDa nuclear protein).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID:8355;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX MEDLINE:94095935; PubMed:9446947;  
RA Schmidt-Zachman M.S., Kroetz S., Kraemer A.;  
RT "Molecular characterization of a novel, widespread nuclear protein  
RL Mol. Biol. Cell 9:143-160(1998).  
CC -!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR A  
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE  
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT  
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS  
CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE  
CC INVOLVED IN THE ASSEMBLY OF THE 70S COMPLEX. BELONGS ALSO TO THE  
CC MINOR U12-DEPENDENT SPLICOSOME WHICH IS INVOLVED IN THE SPLICING  
CC OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON (BY SIMILARITY).  
CC -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED OF  
CC FOUR SUBUNITS: SF3H4/SF419, SF3H1/SAP130, SF352/SAP145,  
CC SF3B1/SAP155. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A  
CC 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN  
CC COMPLEX (U2 SNRNP) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: BELONGS TO THE SF3B1 FAMILY.  
CC -!- SIMILARITY: Contains 2 HEAT REPEATS.

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CC EMBL: X08597; CAA70201.1;  
CC PIR: T30887; T30887.  
CC KW Spliceosome; mRNA processing; mRNA splicing; Nuclear protein;  
CC Repeat.  
SQ SEQUENCE 1307 AA; 146213 MW; 63226C5F3C36C6953 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 1307;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
|||||  
DB 272 GRGDP 277

RESULT 5  
RL7A\_CHICK STANDARD; PRT: 265 AA.

ID RL7A\_CHICK  
AC P32429;  
DT 01-OCT-1993 (Rel. 27, Created)  
DI 01-OCT-1993 (Rel. 27, Last sequence update)  
DI 01-FEB-1996 (Rel. 33, Last annotation update)  
DE 50S ribosomal protein L7a.  
DE RL7A OR SURF-3.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID:9031;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX TISSUE=Liver;  
RX MEDLINE:92335297; PubMed:1631131;  
RA Colombo P., Yon J., Garson K., Fried M.;  
RE "Conservation of the organization of five tightly clustered genes  
RE over 600 million years of divergent evolution".  
RE Proc. Natl. Acad. Sci. U.S.A. 89:6358-6362(1992).  
RN 12;  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE:94100270; PubMed:8274530;  
RA Maeda N., Kenmochi N., Tanaka T.;  
RE "The complete nucleotide sequence of chicken ribosomal protein L7a  
RE gene and the multiple factor binding sites in its 5' flanking  
RE region".  
RE Biochimie 75:785-790(1993).  
CC -!- SIMILARITY: BELONGS TO THE L7AE FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL: X62640; CAA44506.1;  
CC EMBL: D14522; BAA03395.1;  
CC PIR: A46032; S19159.  
CC -!- InterPro: IPR004038; Ribosomal\_L7A.  
CC -!- InterPro: IPR004037; Ribosomal\_L7Ae.  
CC Pfam: PF01248; Ribosomal\_L7Ae; 1.  
CC PRINTS: PR00881; L7ARS6FAMILY.  
CC PROSITE: PS01082; RIBOSOMAL\_L7AE; 1.  
CC KW Ribosomal protein.  
FT INIT\_MET 0  
SQ SEQUENCE 265 AA; 29868 MW; 07E312C639B5655 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 265;  
Best Local Similarity 83.3%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
|||||  
DB 123 GRGDP 128

RESULT 6  
MF22\_ARATH STANDARD; PRT: 458 AA.

ID MF22\_ARATH  
AC O80950;  
DI 16-OCT-2001 (Rel. 40, Created)  
DI 16-OCT-2001 (Rel. 40, Last sequence update)  
DI 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Myosinase binding protein-like Atg39310.  
DE ATG39310 OR T16B24.5.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC



CC NCBI\_TaxID-4932;  
 CC [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-S2886//AB972;  
 RC Pubmed-9289976;  
 RA Churchev C.M., Bowman S., Badcock K., Backler A., Brown L.,  
 RA Chillingworth I., Connor R., Devlin K., Gentles S., Hamlin N.,  
 RA Harris D.E., Horsnell T., Hunt S., Jajels K., Jones M., Iye G.,  
 RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,  
 RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,  
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";  
 RJ Nature 387:84-87(1997).  
 CC -!- SIMILARITY: TO YEAST DIPHTERIA TOXIN RESISTANCE PROTEIN 2 (PF52).  
 CC TO S.POMBE SPAC13F4.152, SPBC3B9.05, TO C.ELEGANS C09G5.2, C1451.5  
 CC AND M.JANNASCHII M30483.  
 CC -----  
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 CC -----  
 DR EMBL: Z56125; CAAB5277.1; -  
 DR PIR: S48469; S48469.  
 DR SGD: S0001365; Y11103W.  
 DR InterPro: IPR002728; Diphtheramide\_syn.  
 DR Pfam: PF01866; Diphtheramide\_syn.1.  
 DR ProDom: PD084399; Diphtheramide\_syn.1.  
 DR TIGRFAMs: TIGR00322; diphthb2\_k1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 425 AA; 46310 MW; 24E93852E3376722 CRC64;  
 Query Match 89.6%; Score 31; DP 1; Length 425;  
 Best Local Similarity 83.3%; Pred. No. 28;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGETP 6  
 DB 415 GRGETP 425  
 11111  
 RESULT 9  
 Y463.SYNV3  
 ID Y863.SYNV3 STANDARD: PRT; 453 AA.  
 AC P73754;  
 DI 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein slr0863.  
 GN SLR0863.  
 OS Synchocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
 OX NCBI\_TaxID-1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97061201; PubMed-8905241;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizi E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Suikura H., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nairo K.,  
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.,  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synchocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL Res. 3:109-116(1995).  
 CC -!- SIMILARITY: BELONGS TO THE TLCD/PMBA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L90509; BAA17806.1; -  
 DR PIR: S74845; S74845.  
 DR InterPro: IPR002510; PMBA\_TLCD.  
 DR Pfam: PF01523; PMBA\_TLCD.1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 463 AA; 50369 MW; 220173C7C5A42D CRC64;  
 Query Match 88.6%; Score 31; DP 1; Length 463;  
 Best Local Similarity 83.3%; Pred. No. 31;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGETP 6  
 DB 352 GRGETP 357  
 11111  
 RESULT 10  
 P1NC.CHICK  
 ID P1NC.CHICK STANDARD: PRT; 1255 AA.  
 AC P11722; O90921;  
 DI 01-OCT-1989 (Rel. 12, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibronectin (FN) (Fragments).  
 GN FN1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neornithes; Galliformes; Phasianidae; Phasianinae;  
 OX Gallus.  
 OX NCBI\_TaxID-9031;  
 RN [1]  
 RP SEQUENCE OF 1-50 FROM N.A.  
 RX MEDLINE-83117850; PubMed-6572007;  
 RA Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,  
 RA Yamada K.M.,  
 RT "Isolation of genomic DNA clones spanning the entire fibronectin  
 RT gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).  
 RN [2]  
 RP SEQUENCE OF 51-1256 FROM N.A.  
 RC STRAIN-White leghorn;  
 RC Norton P.A.;  
 RC Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 227-415 FROM N.A.  
 RX MEDLINE-96183658; PubMed-8603103;  
 RA Gehris A.L., Brandli D.W., Lewis S.D., Bennett V.D.;  
 RT "The exon encoding the fibronectin type III-4 repeat is  
 RT constitutively included in the mRNA from chick limb mesenchyme and  
 RT cartilage.";  
 RL Biochim. Biophys. Acta 1311:5-12(1996).  
 RN [4]  
 RP SEQUENCE OF 327-599 FROM N.A.  
 RX MEDLINE-83050950; PubMed-2823899;  
 RA Kubomura S., Obara M., Karasaki Y., Taniguchi H., Gotoh S.,  
 RA Tsuda T., Higashi K., Ohsato K., Hiaro H.;  
 RT "Genetic analysis of the cell binding domain region of the chicken  
 RT fibronectin gene.";  
 RL Biochim. Biophys. Acta 910:171-181(1997).  
 RN [5]  
 RP SEQUENCE OF 413-1256 FROM N.A.  
 RX MEDLINE-88142820; PubMed-2830457;  
 RA Norton P.A., Hynes R.O.;  
 RT "Alternative splicing of chicken fibronectin in embryos and in normal  
 RT and transformed cells.";  
 RL Mol. Cell. Biol. 7:4297-4307(1987).  
 CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, DIFFERENTIATION, WOUND





FT DOMAIN 568 557 FIBRONECTIN TYPE-III (EXTRA DOMAIN).  
 FT DOMAIN 658 749 FIBRONECTIN TYPE-III.  
 FT DOMAIN 750 838 FIBRONECTIN TYPE-III.  
 FT DOMAIN 839 929 FIBRONECTIN TYPE-III.  
 FT DOMAIN 930 1264 CONNECTING STRAND 3 (CS-3) (V REGION).  
 FT DOMAIN 1265 1143 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1155 1199 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1200 1243 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1245 1287 FIBRONECTIN TYPE-III.  
 FT DISULFID 1157 1186 BY SIMILARITY.  
 FT DISULFID 1184 1196 BY SIMILARITY.  
 FT DISULFID 1202 1229 BY SIMILARITY.  
 FT DISULFID 1227 1249 BY SIMILARITY.  
 FT DISULFID 1247 1270 BY SIMILARITY.  
 FT DISULFID 1266 1284 BY SIMILARITY.  
 FT DISULFID 1320 1320 INTERCHAIN (WITH 1324 OF OTHER CHAIN). (BY SIMILARITY).  
 FT DISULFID 1324 1324 INTERCHAIN (WITH 1320 OF OTHER CHAIN). (BY SIMILARITY).  
 FT SITE 461 463 CELL ATTACHMENT SITE.  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC...) (POENTIAL)  
 SQ SEQUENCE 1328 AA: 145537 MW: 63157966 DALI 674 CRO64;  
 Query Match 85.6%; Score 31; DB 1; Length 1328;  
 Host Local Similarity 63.1%; Pred. No. 95;  
 Matches 5; Conservative 13; Mismatches 0; Gaps 0;  
 QY 1 GRSTPT 6  
 D5 460 GGDNP 465  
 ID FINE BOVIN STANDARD; PRI: 2265 AA.  
 AC P07589;  
 DT 01-APR-1988 (Sci. 37, Created;  
 DT 01-SEP-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibronection (FN).  
 GN FN1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 CX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=87054047; PubMed=3780752;  
 RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;  
 RT "Complete primary structure of bovine plasma fibronection";  
 RL Eur. J. Biochem. 161:441-453(1986).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RX MEDLINE=83117605; PubMed=6218503;  
 RA Petersen T.E., Thorgeresen H.C., Skorstengaard K., Vibe-Pedersen K.,  
 RA Sahl P., Sottrup-Jensen L., Magnusson S.;  
 RT "Partial primary structure of bovine plasma fibronection: three types  
 of internal homology";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).  
 RN [3]  
 RP SEQUENCE OF 2170-2265 FROM N.A.  
 RX MEDLINE=83221567; PubMed=6104699;  
 RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;  
 RT "Isolation and characterization of cDNA clones for human and bovine  
 fibronectins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).  
 CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPONENTS  
 INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND  
 HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -1- SURUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED  
 VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;

CC TO A LESSER EXTEND HOMODIMERS.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing: Named isoforms=1;  
 CC Comment=A number of isoforms are produced. Each of the "extra  
 CC domain" and the connecting strand 3 are present in some forms of  
 CC fibronectin and absent in others;  
 CC Name=1;  
 CC IsoId=P07589.1; Sequence=Displayed;  
 CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED  
 CC BY HEPATOCYTES. CELLULAR FN (OLIGOMERIC OR CROSS-LINKED MULTIMERIC  
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.  
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.  
 CC -1- SIMILARITY: Contains 15 fibronectin type III domains.  
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 CC FMBL: K09800; AAA30521.2;  
 CC FTR: A26452; FNBO.  
 CC HSSP: P02751; 2FN2.  
 CC InterPro: IPR004209; EGF-like.  
 CC InterPro: IPR003083; Fibrinectin.  
 CC InterPro: IPR003961; FN\_III.  
 CC InterPro: IPR000562; FN\_Type\_III.  
 CC InterPro: IPR003962; FN\_III\_sulf.  
 CC Pfam: PF00039; fn1; 12.  
 CC Pfam: PF00040; fn2; 2.  
 CC Pfam: PF00041; fn3; 15.  
 CC PRINTS: PR00013; FNTYPEIII.  
 CC PRINTS: PR00014; FNTYPEIII.  
 CC PRODOM: PD000995; FN\_Type\_III; 2.  
 CC SMART: SMC0058; FN1; 12.  
 CC SMART: SMC0059; FN2; 2.  
 CC SMART: SMC0060; FN3; 14.  
 CC PROSITE: PS00022; EGF\_1; 2.  
 CC PROSITE: PS00023; FIBRONECTIN\_2; 2.  
 CC PROSITE: PS01253; FIBRONECTIN\_1; 12.  
 CC Glycoprotein: Plasma; Heparin-binding; Acute phase; Phosphorylation;  
 CC Sulfation; Cell adhesion; Repeat; Alternative splicing;  
 CC Pyroglutamate carboxylic acid.  
 CC MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 CC FT DOMAIN 21 241 FIBRIN- AND HEPARIN-BINDING 1.  
 CC FT DOMAIN 277 577 COLLAGEN-BINDING.  
 CC FT DNA\_BIND 876 1141 CELL-ATTACHMENT.  
 CC FT DOMAIN 1236 1509 HEPARIN-BINDING 2.  
 CC FT DOMAIN 1600 1870 FIBRIN-BINDING 2.  
 CC FT DOMAIN 1991 2216 FIBRONECTIN TYPE-I 1.  
 CC FT DOMAIN 19 59 FIBRONECTIN TYPE-I 2.  
 CC FT DOMAIN 64 107 FIBRONECTIN TYPE-I 3.  
 CC FT DOMAIN 108 151 FIBRONECTIN TYPE-I 4.  
 CC FT DOMAIN 153 197 FIBRONECTIN TYPE-I 5.  
 CC FT DOMAIN 198 242 FIBRONECTIN TYPE-I 6.  
 CC FT DOMAIN 275 314 FIBRONECTIN TYPE-I 1.  
 CC FT DOMAIN 314 373 FIBRONECTIN TYPE-I 2.  
 CC FT DOMAIN 374 438 FIBRONECTIN TYPE-I 3.  
 CC FT DOMAIN 437 480 FIBRONECTIN TYPE-I 4.  
 CC FT DOMAIN 485 527 FIBRONECTIN TYPE-I 8.  
 CC FT DOMAIN 528 571 FIBRONECTIN TYPE-I 9.  
 CC FT DOMAIN 578 669 FIBRONECTIN TYPE-III 1.  
 CC FT DOMAIN 668 778 FIBRONECTIN TYPE-III 2.  
 CC FT DOMAIN 779 874 FIBRONECTIN TYPE-III 3.  
 CC FT DOMAIN 875 964 FIBRONECTIN TYPE-III 4.  
 CC FT DOMAIN 965 1054 FIBRONECTIN TYPE-III 5.  
 CC FT DOMAIN 1055 1141 FIBRONECTIN TYPE-III 6.  
 CC FT DOMAIN 1142 1234 FIBRONECTIN TYPE-III 7.

FT	DOMAIN	1235	1325	FIBRONECTIN TYPE-11 9.	FE	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
FT	DOMAIN	1326	1475	FIBRONECTIN TYPE-11 9.	FN	FN1 OR FN.
FT	DOMAIN	1416	1504	FIBRONECTIN TYPE-11 9.	S	Homo sapiens (Human).
FT	DOMAIN	1510	1599	FIBRONECTIN TYPE-11 11 (EXTRA DOMAIN).	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
FT	DOMAIN	1600	1631	FIBRONECTIN TYPE-11 12.	MC	Mammalia; Eutheraia; Primates; Catarrhini; Hominoidea;
FT	DOMAIN	1692	1733	FIBRONECTIN TYPE-11 14.	OX	NCBI_taxid-9606;
FT	DOMAIN	1781	1879	FIBRONECTIN TYPE-11 14.	FN	[1]
FT	DOMAIN	1871	1990	CONNECTING STRAND 1 (CS 1) (V FIBRONECTIN).	EP	SEQUENCE OF 1-38 FROM N.A.
FT	DOMAIN	1982	2061	FIBRONECTIN TYPE-11 11.	FX	MEDLINE-87030890; PubMed-370189;
FT	DOMAIN	2083	2127	FIBRONECTIN TYPE-11 12.	FA	Sulman A., Yamada K.M., Kornblitt A.R.;
FT	DOMAIN	2128	2171	FIBRONECTIN TYPE-11 11.	ET	"Human fibronectin is synthesized as a pro-peptidylpropeptide."
FT	DOMAIN	2172	2215	FIBRONECTIN TYPE-11 12.	K.	FEBS Lett. 207:145-148(1986).
FT	SITE	1433	1495	CELL ATTACHMENT SITE	FN	[2]
FT	DISULFID	21	47		EP	SEQUENCE OF 1-49 FROM N.A.
FT	DISULFID	45	56		FX	MEDLINE-8717578; PubMed-3041556;
FT	DISULFID	66	94		FA	Dean D.C., Bowles C.L., Bourgeois S.;
FT	DISULFID	92	184		ET	"Cloning and analysis of the promoter region of the human fibronectin gene."
FT	DISULFID	116	118		ET	Proc. Natl. Acad. Sci. U.S.A. 84:1875-1880(1987).
FT	DISULFID	136	148		FN	[3]
FT	DISULFID	153	194		EP	SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.
FT	DISULFID	182	194		FX	MEDLINE-85284965; PubMed-2992939;
FT	DISULFID	200	229		FA	Kornblitt A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
FT	DISULFID	227	239		ET	"Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene."
FT	DISULFID	302	311		ET	EMBO J. 4:1755-1759(1985).
FT	DISULFID	323	355		FN	[4]
FT	DISULFID	343	370		FN	[5]
FT	DISULFID	383	415		RP	SEQUENCE OF 1594-2386 FROM N.A.
FT	DISULFID	403	440		FX	MEDLINE-8472258; PubMed-6462919;
FT	DISULFID	439	467		FA	Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;
FT	DISULFID	465	477		ET	"Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats."
FT	DISULFID	487	514		ET	Nucleic Acids Res. 12:5853-5866(1984).
FT	DISULFID	512	524		FN	[6]
FT	DISULFID	530	558		RP	SEQUENCE OF 1594-2386 FROM N.A.
FT	DISULFID	556	568		FX	MEDLINE-85280409; PubMed-2992573;
FT	DISULFID	2085	2114		RA	Hernard M.P., Kolbe M., Weil D., Chu M.-L.;
FT	DISULFID	2124	2124		ET	"Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions."
FT	DISULFID	2155	2167		ET	J. Biochem. 258:12670-12674(1983).
FT	DISULFID	2174	2230		FN	[7]
FT	DISULFID	2198	2205		EP	SEQUENCE OF 309-608, AND COLLAGEN-5INCLING.
FT	DISULFID	2246	2246		FX	MEDLINE-87080265; PubMed-3024962;
FT	DISULFID	2250	2250		FA	Owens R.J., Baralle F.E.;
FT	MOD_RES	845	845		ET	"Mapping the collagen-binding site of human fibronectin by expression of the NH2-terminal domain."
FT	MOD_RES	850	850		ET	J. Biol. Chem. 258:12670-12674(1983).
FT	CARBOHYD	399	399		FN	[8]
FT	CARBOHYD	497	497		FX	MEDLINE-84032463; PubMed-6530202;
FT	CARBOHYD	511	511		FA	Garcia-Pardo A., Pearlstein E., Franciose B.;
FT	CARBOHYD	546	546		ET	"Primary structure of human plasma fibronectin. The 29,000 dalton NH2-terminal domain."
FT	CARBOHYD	974	974		FN	[9]
FT	CARBOHYD	1213	1213		FX	MEDLINE-87080265; PubMed-3024962;
FT	CARBOHYD	1987	1987		FA	Owens R.J., Baralle F.E.;
FT	CARBOHYD	1943	1943		ET	"Mapping the collagen-binding site of human fibronectin by expression of the NH2-terminal domain."
FT	CARBOHYD	1944	1944		ET	EMBO J. 5:2825-2830(1986).
FT	MOD_RES	2263	2263		FN	[10]
FT	SEQUENCE	2265	2265		FX	MEDLINE-82265604; PubMed-7050098;
FT	SEQUENCE	2265	2265		FA	Pierischbacher M.D., Ruoslahti E., Suckling J., Lind P., Peterson P.A.;
FT	SEQUENCE	2265	2265		ET	"The cell attachment domain of fibronectin. Determination of the primary structure."
FT	SEQUENCE	2265	2265		ET	J. Biol. Chem. 257:9593-9597(1982).
FT	SEQUENCE	2265	2265		FN	[9]
FT	SEQUENCE	2265	2265		FX	MEDLINE-83290929; PubMed-6688418;
FT	SEQUENCE	2265	2265		FA	Oldberg A., Linney E., Ruoslahti E.;
FT	SEQUENCE	2265	2265		ET	"Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell attachment domain in human fibronectin."
FT	SEQUENCE	2265	2265		ET	J. Biol. Chem. 258:10193-10196(1983).
FT	SEQUENCE	2265	2265		FN	[10]
FT	SEQUENCE	2265	2265		FX	MEDLINE-86111901; PubMed-3003995;
FT	SEQUENCE	2265	2265		FA	Oldberg A., Ruoslahti E.;

Query Match 88.6%; Score 31; 55 11; Length 2265;

Best Local Similarity 81.3%; Pred. No. 1,40-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

|||||

Db 1492 GRGDP 1497

RESULT 13

FIND\_HUMAN STANDARD; PK: 2386 AA.

AC P02751; Q14726; Q9H188;

DT 21-JUL-1986 (Ref. 01, Created);

DT 01-NOV-1997 (Ref. 35, Last sequence update)

DT 15-SEP-2003 (Ref. 42, Last annotation update)

RT \*Evolution of the fibronectin gene. Exon structure of cell attachment  
 RL domain".  
 RN J. Biol. Chem. 261:2113-2116(1986).  
 RN [11]  
 RP SEQUENCE OF 1712-1739 FROM N.A.  
 RX MEDLINE-87026578; PubMed-7021206;  
 RA Sekiguchi K., Kios A.M., Kurachi K., Yoshitake S., Hakomori S.  
 RT \*Human liver fibronectin complementary DNAs: Identification of two  
 RT different messenger RNAs possibly encoding the alpha and beta  
 RT subunits of plasma fibronectin".  
 RL Biochemistry 25:4536-4541(1986).  
 RN [12]  
 RP SEQUENCE FROM N.A. (1500-1600 Z).  
 RX Schor S.F., Schor A.M., Senecviratne K., Kay R., Ellis J., Bailly E.,  
 SA Clausen J.  
 RT \*Migration stimulating factor (MSF): a novel transcription variant of  
 RT the fibronectin gene".  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBS databases.  
 RN [13]  
 RP SULFATION.  
 RX MEDLINE-86042625; PubMed-2413772;  
 RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.  
 RT \*Tyrosine sulfation of proteins from the human hepatoma cell line  
 RT HepG2".  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).  
 RN [14]  
 RP FBLN1-BINDING SITE.  
 RX PubMed-1420349;  
 RA Baibona K., Tran H., Gadya S., Ingham K.C., Strickland D.K.,  
 RA Argraves W.S.  
 RT \*Fibulin binds to itself and to the carboxyl-terminal heparin-binding  
 RT region of fibronectin".  
 RL J. Biol. Chem. 267:20120-20125(1992).  
 RN [15]  
 RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.  
 RX MEDLINE-95081153; PubMed-7389359;  
 RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.L.  
 RT \*Further characterization of the NH2-terminal fibrin-binding site in  
 RT fibronectin".  
 RL J. Biol. Chem. 269:31938-31945(1994).  
 RN [16]  
 RP STRUCTURE BY NMR OF 32-92.  
 RX MEDLINE-96069779; PubMed-7583666;  
 RA Potts J.R., Phan I., Williams M.J., Campbell I.D.  
 RT \*High-resolution structural studies of the factor XIIIa crosslinking  
 RT site and the first type 1 module of fibronectin".  
 RL Nat. Struct. Biol. 2:946-950(1995).  
 RN [17]  
 RP STRUCTURE BY NMR OF 182-275.  
 RX MEDLINE-9444923; PubMed-6308892;  
 RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.L.,  
 RA Campbell I.D.  
 RT \*Solution structure of a pair of fibronectin type 1 modules with  
 RT fibrin binding activity".  
 RL J. Mol. Biol. 235:1302-1311(1994).  
 RN [18]  
 RP STRUCTURE BY NMR OF 406-464.  
 RX MEDLINE-98179558; PubMed-9514732;  
 RA Sticht H., Pickford A.R., Potts J.R., Campbell I.D.  
 RT \*Solution structure of the glycosylated second type 2 module of  
 RT fibronectin".  
 RL J. Mol. Biol. 276:177-187(1998).  
 RN [19]  
 RP STRUCTURE BY NMR OF 1447-1540.  
 RX MEDLINE-93046665; PubMed-1423622;  
 RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.  
 RT \*The three-dimensional structure of the tenth type II module of  
 RT fibronectin: an insight into RGD-mediated interactions".  
 RL Cell 71:671-678(1992).  
 RN [20]  
 RP STRUCTURE BY NMR OF 1447-1540.  
 RX MEDLINE-92162710; PubMed-1111202;  
 RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,

RA Campbell I.D.  
 RT \*1H NMR assignment and secondary structure of the cell adhesion type  
 RL III module of fibronectin".  
 RN Biochemistry 31:2068-2073(1992).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1545.  
 RX MEDLINE-94166075; PubMed-8120888;  
 RA Dickinson C.D., Veerapandian B., Dai X.-P., Hamlin R.C., Xuong N.-H.,  
 RA Ruoslahti E., Ely K.R.  
 RT \*Crystal structure of the tenth type III cell adhesion module of  
 RT human fibronectin".  
 RL J. Mol. Biol. 236:1079-1092(1994).  
 RN [22]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1721-1991.  
 RX MEDLINE-99177162; PubMed-10075919;  
 RA Sharma A., Askari J.A., Humphries M.J., Jones E.Y., Stuart D.L.  
 RT \*Crystal structure of a heparin- and integrin-binding segment of human  
 RT fibronectin".  
 RL EMBO J. 18:1468-1479(1999).  
 CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, ORGANOIZATION, WOUND  
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced  
 CC variants, connected by 2 disulfide bonds near the carboxyl ends;  
 CC to a lesser extent homodimers. Interacts with FBLN1.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing: Named isoforms 2;  
 CC Comment-Additional isoforms seem to exist;  
 CC Name: 1;  
 CC IsoId: P02751-1; Sequence-Displayed;  
 CC Names: 2; Synonyms-MSF-FN70, Migration stimulation factor FN70;  
 CC IsoId: P02751-2; Sequence-VSP\_003255, VSP\_003256, VSP\_003257;  
 CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE D-MERIC FORM) IS SECRETED  
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC  
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 CC -1- PTM: SULFATED.  
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.  
 CC -1- SIMILARITY: Contains 4 fibronectin type II domains.  
 CC -1- SIMILARITY: Contains 16 fibronectin type III domains.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 Query Match 88.6%; Score 31; DB 1; Length 2386;  
 Best Local Similarity 83.3%; Prod. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GRGDTP 6  
 Eb 1523 GRGDSP 1528  
 RESULT 14  
 FINC\_MOUSE  
 ID FINC\_MOUSE STANDARD; PRT: 2477 AA.  
 AC P11276; O61567; O61568; O61569; O64233;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DE 01-NOV-1997 (Rel. 35, Last sequence update)  
 DI 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibronectin precursor (FN) (Fragments).  
 GN FNI.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 GN NCBI\_TaxID=10090;  
 RN [1]

SEQUENCE OF 1-28 FROM N.A.  
 TISSUE=Ovary;  
 MEDLINE=9413133; PubMed=6293772;  
 RA Polly P., Nicolson R.C.;  
 R2 "Sequence of the mouse fibronectin-encoding gene promoter region";  
 AL Gene 137:353-354(1993).  
 RN [2]  
 RN RP SEQUENCE OF 562-684 FROM N.A.  
 RN RC STRAIN=NMRI;  
 RN RX MEDLINE=95403556; PubMed=7673345;  
 RA Talts J.F., Weller A., Timp R., Ekblom M., Ekblom P.;  
 R1 "Regulation of mesenchymal extracellular matrix protein synthesis by  
 R2 transforming growth factor-beta and glucocorticoids in human  
 R3 stroma";  
 RL J. Cell Sci. 106:2153-2162(1995).  
 RN [3]  
 RN RP SEQUENCE OF 890-2476 FROM N.A.  
 RN RA Gorski G., Aros M., Norton P.;  
 RN R1 Submitted (DEC-1995) to the EMBL/GenBank/SDBJ Databases.  
 RN [4]  
 RN RP SEQUENCE OF 2375-2477 FROM N.A.  
 RN RX MEDLINE=98124987; PubMed=3124113;  
 RA Blatti S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;  
 R1 "Induction of fibronectin gene transcription and mRNA is a primary  
 R2 response to growth-factor stimulation of AKR-2B cells";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).  
 RN [5]  
 RN RP SEQUENCE OF 2375-2477 FROM N.A.  
 RN RC TISSUE=Kidney;  
 RN RX MEDLINE=93011702; PubMed=1327655;  
 RA Khandjian E.W., Salomon C., Leonard N., Tremblay S., Turley H.;  
 R1 "Fibronectin gene expression in proliferating, quiescent, and SV40-  
 R2 infected mouse kidney cells";  
 RL Exp. Cell. Res. 202:464-476(1992).  
 RN [6]  
 RN RP STRUCTURE BY NMR OF 1447-1636.  
 RN RX MEDLINE=96202578; PubMed=9533887;  
 RA Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,  
 R1 Pastor R.W., Krueger S., Torchia D.A.;  
 R2 "Solution structure and dynamics of linked cell attachment modules of  
 R3 mouse fibronectin containing the RGD and synergy regions: comparison  
 R4 with the human fibronectin crystal structure";  
 RL J. Mol. Biol. 277:663-682(1998).  
 RN [7]  
 RN RP DOWN-REGULATION BY GLUCOCORTICOLS.  
 RN RX PubMed=1137251;  
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;  
 R1 "Glucocorticoids down-regulate the extracellular matrix proteins  
 R2 fibronectin, fibrin-1 and fibrin-2 in bone marrow stroma";  
 RL Eur. J. Haematol. 67:176-184(2001).  
 CC -1- FUNCTION: FIBRONECTIN BINDS CELL SURFACES AND VARIOUS COMPONENTS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, REGENERATION, WOUND  
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced  
 CC variants, connected by 2 disulfide bonds near the carboxyl ends;  
 CC to a lesser extent homodimers. Interacts with FBN1 (3)  
 CC similarity;  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing: Named isoforms-1;  
 CC Comment-A number of isoforms are produced. Each of the "extra  
 CC domain" and the connecting strand 3 are present in some forms of  
 CC fibronectin and absent in others;  
 CC Name=1;  
 CC IsoId=P11276-1; Sequence=displayed;  
 CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED  
 CC BY HEPATOCYTES, CELLULAR FN (OLIGOMER OR CROSS-LINKED MULTIMERIC  
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 CC -1- INDUCTION: Glucocorticoids suppress mRNA expression and protein  
 CC synthesis.  
 CC -1- PTM: SULFATED (BY SIMILARITY).  
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.  
 CC  
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.  
 CC -1- SIMILARITY: Contains 17 fibronectin type III domains.  
 CC  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 18:14:22 : Search time 34 seconds

(without alignments)  
46,919 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGDT 6

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Searched: 53025 seqs, 25052604 residues

Total number of hits satisfying chosen parameters: 53025

Minimum DB seq length: 6

Maximum DB seq length: 260000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMAL\_23\*

1: SP archaea\*

2: SP bacteria\*

3: SP fungi\*

4: SP mammals\*

5: SP invertebrate\*

6: SP plants\*

7: SP algae\*

8: SP archaea\*

9: SP plants\*

10: SP plants\*

11: SP rodents\*

12: SP viruses\*

13: SP vertebrate\*

14: SP unclassified\*

15: SP viruses\*

16: SP bacteria\*

17: SP archaea\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	354	5 Q9B110	Q9B110 Bombyx mori
2	35	100.0	450	16 Q9AA55	Q9AA55 Caenorhabditis
3	35	100.0	490	11 Q9CK55	Q9CK55 Mus musculus
4	35	100.0	496	11 Q9ET34	Q9ET34 Rattus norvegicus
5	35	100.0	1209	5 Q8T8C0	Q8T8C0 Bombyx mori
6	32	91.4	458	10 Q8TAD2	Q8TAD2 Arabidopsis
7	32	91.4	606	15 Q8YKQ0	Q8YKQ0 Anabaena sp
8	31	88.6	23	4 Q9UC00	Q9UC00 Homo sapiens
9	31	88.6	86	2 Q9E2D2	Q9E2D2 Rhabdium m
10	31	88.6	185	8 Q8HUM8	Q8HUM8 Woodwardia
11	31	88.6	185	6 Q8HUM7	Q8HUM7 Woodwardia
12	31	88.6	185	3 Q8HUM2	Q8HUM2 Woodwardia
13	31	88.6	208	16 Q8ZK28	Q8ZK28 Rhabdium m
14	31	88.6	218	4 Q8N290	Q8N290 Homo sapiens
15	31	88.6	275	16 Q92BA3	Q92BA3 Rhabdium m
16	31	88.6	293	6 Q9XSG0	Q9XSG0 Corynebacte

17	31	88.6	301	11 Q8C0C1	Q8C0C1 Mus musculus
18	31	88.6	363	11 Q8CC85	Q8CC85 Mus musculus
19	31	88.6	399	17 Q9HQ14	Q9HQ14 Halobacteri
20	31	88.6	407	8 Q8SGBC	Q8SGBC Micropterus
21	31	88.6	438	2 Q9X2S7	Q9X2S7 Vibrio chol
22	31	88.6	438	16 Q9KNL9	Q9KNL9 Vibrio chol
23	31	88.6	441	17 Q9HON2	Q9HON2 Halobacteri
24	31	88.6	515	16 Q8X5B0	Q8X5B0 Escherichia
25	31	88.6	515	16 Q8FKR9	Q8FKR9 Escherichia
26	31	88.6	562	4 Q8NC49	Q8NC49 Homo sapien
27	31	88.6	589	13 Q8OYL3	Q8OYL3 Brachydanio
28	31	88.6	606	5 Q18869	Q18869 Caenorhabdi
29	31	88.6	618	17 Q8TYO5	Q8TYO5 Methacopryc
30	31	88.6	659	10 Q8GWM7	Q8GWM7 Arabidopsis
31	31	88.6	686	11 Q8GSH5	Q8GSH5 Mus musculus
32	31	88.6	686	11 Q8H24	Q8H24 Mus musculus
33	31	88.6	691	10 Q8M334	Q8M334 Arabidopsis
34	31	88.6	1105	5 Q9VX44	Q9VX44 Drosophila
35	31	88.6	1169	5 Q9VX45	Q9VX45 Drosophila
36	31	88.6	1174	5 Q8MOX9	Q8MOX9 Drosophila
37	33	88.6	2478	13 Q93406	Q93406 Brachydanio
38	30	85.7	138	15 Q9Z277	Q9Z277 Chimpazee
39	30	85.7	144	11 Q8C3E1	Q8C3E1 Mus musculus
40	30	85.7	161	11 Q8CV77	Q8CV77 Mus musculus
41	30	85.7	181	16 Q8ZK15	Q8ZK15 Rhabdium m
42	30	85.7	192	16 Q8NPQ8	Q8NPQ8 Corynebacte
43	30	85.7	207	16 Q8N721	Q8N721 Corynebacte
44	30	85.7	231	5 Q9GQ16	Q9GQ16 Caenorhabdi
45	30	85.7	247	3 Q9C1R3	Q9C1R3 Emmericella

#### ALIGNMENTS

#### RESULT 1

Q9C1G Q9B110 PRELIMINARY: PWT: 354 AA.  
AC Q9B110  
DE 31-JUN-2001 (TrEMBLrel. 17, Created)  
DE 31-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 31-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Inducible nitric oxide synthase-like protein (INOS-LP)  
DE (Fragment).  
GN INOS-LP.  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
OC Bombycidae; Bombyx.  
OX NCBI\_TaxID:7091.  
RN [1]  
RP SEQUENCE FROM N.A.  
SA Yang J., Taitai K., Yanakawa M.,  
RC "Inducible nitric oxide synthase-like protein (INOS-LP) cDNA."  
RC Submitted (SEP-1998) to the EMBL/GenBank/USF databases.  
DR EMBL: AB017521; BAB33296.1; -.  
DR HSSP: P29477; INOC.  
DR InterPro: IPR004030; NO\_synthase.  
DR Pfam: PF02898; NO\_synthase; -.  
DR PROSITE: PS00001; NOS: 1.  
FT NON\_TER 354 354  
SQ SEQUENCE 354 AA; 40804 MW; 8D76BA87H739F9A CRC64;

Query Match 100.0%; Score 35; DB 5; Length 354;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : GRGDT 6

DB : 109 GRGDT 114

#### RESULT 2

Q9AA55

Q9AA55 PRELIMINARY: PRI: 450 AA.  
 Q9AA55: 01-JUN-2001 (TrEMBLrel. 17, Created)  
 AC 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Multidrug resistance protein, putative  
 DE CC0751.  
 GN Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_TaxID=55892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13089 / CR15;  
 RC MEDLINE=21173598; PubMed=11256447;  
 RA Eisen J., Heideberg J.F., Alley M.K., Chla H., Mallick D.P., Fly B.,  
 RA Potocka L., Nelson W.C., Newton A., Stephens J., Madke D.H.,  
 RA DeBoy R.T., Dodson R., Durkin A.S., Gwinn M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Smit M.B., Khouri R., Shetty J., Berry K.,  
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 VT "Complete genome sequence of Caulobacter crescentus";  
 RL Proc. Natl. Acad. Sci. USA. 98:4336-4341;2001;  
 RL EMBL: A0005751; AAK22716.1;  
 RL TIGR: CC0751;  
 DR InterPro: IPR001958; TOR\_TOLA.  
 DR PRINTS: PR01035; TCRTETA.  
 DR PROSITE: PS03850; MFS: 1.  
 DR Complete proteome.  
 SK SEQUENCE 450 AA; 46965 MW; 6577B79F6F5892 CRC64;  
 Query Match 100.0%; Score 35; DB 16; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 220 GRGDTP 225  
 [11111]  
 PRELIMINARY: PRI: 490 AA.  
 AC Q9CSX5;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 AC Q9CSX5: 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE 2810001MCSRIK protein (Fragment).  
 DE SF3B1 OR 2810001M05RIK.  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshida M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kozuka H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosaka H., Kondo S., Yamagata S.,  
 RA Saito T., Okazaki Y., Gotohori T., Hono H., Kasukawa T., Saifu M.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Ratalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glaziou C., Kirn B., Kishida H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nishida T., Pesole G., Glocker-Gush J.,  
 RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washie I.,  
 RA Sakai K., Orido T., Furuno M., Aono H., Balkarali F., Bartsch G.,  
 RA Blake J., Seifell J., de Bejanda N., Carinci P., de Benedic M.F.,  
 RA Brownstein M.J., Rult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee K.H.,  
 RA Lyons P., Marconcioni L., Mashima J., Mazzarelli J., Mombacchi P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

SA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz G., Whittaker G., Williams L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kozsaki S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:585-599(2001);  
 DE EMBL: AK012632; BAE28365.1;  
 DE MCD: MCD:1932339; Sfl3b1.  
 DE NON\_TER 490 490  
 FT NON\_TER 490 AA; 53634 MW; F326E5C92B707F3 CRC64;  
 SQ SEQUENCE 490 AA; 53634 MW; 5175C3E304272557 CRC64;  
 Query Match 100.0%; Score 35; DB 11; Length 490;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 269 GRGDTP 274  
 [11111]  
 PRELIMINARY: PRI: 496 AA.  
 AC Q9ET34;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 AC Q9ET34: 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Spliceosomal protein SAPI55 (Fragment).  
 DE Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Costain W.J., Mishra R.K.;  
 RT "Identification and cloning of rat SAPI55 homolog";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DE EMBL: AF260435; AAG01404.1;  
 DE NON\_TER 496 496  
 FT NON\_TER 496 AA; 54496 MW; 5175C3E304272557 CRC64;  
 SQ SEQUENCE 496 AA; 54496 MW; 5175C3E304272557 CRC64;  
 Query Match 100.0%; Score 35; DB 11; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 269 GRGDTP 274  
 [11111]  
 PRELIMINARY: PRI: 1239 AA.  
 AC Q818CU;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 AC Q818CU: 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Nitric oxide synthase.  
 DE BNMO5.  
 OC Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Lepidoptera;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Imamura M., Yang J., Yamakawa M.;  
 RT "cDNA cloning, characterization and gene expression of nitric oxide  
 RT synthase from the silkworm, Bombyx mori";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DE EMBL: AB071182; BAB5836.1;  
 DE InterPro: IPR003097; FAD\_binding.



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DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR004030; NO-synthase.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding_1.
DR Pfam: PF00258; flavodoxin.
DR Pfam: PF00175; NAD_binding_1.
DR Pfam: PF02858; NO-synthase.
DR PROSITE: PS00601; NOS.
SQ SEQUENCE 1209 AA: 137506 MW: 52A73E04B1262E2C CRC64:

Query Match 100.0%; Score 35; DB 5; Length 1209;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 109 GRGDTP 114

RESULT 6
Q8LBD2 PRELIMINARY: PRT; 458 AA.
ID Q8LBD2
AC Q8LBD2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Putative myrosinase-binding protein.
DE Arabidopsis thaliana (Mouse ear cross).
DE Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Malvales; Brassicaceae; Arabidopsis.
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID:3702;
RN [1]
SQ SEQUENCE FROM N.A.
RA Haas R.J., Volkovskiy N., Town C.D., Zerkovskiy M., Alexandrov K.,
RA Feldmann K.,
RA Submitted (MAR-2002) to the EMBL/GenBank/CCDB Databases.
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE "Full-length messenger RNA sequences greatly improve genome
DE annotation."
RI Genome Biol. 3:3-0(2002).
RL [2]
SQ SEQUENCE FROM N.A.
RA Brover V., Trukhan M., Alexandrov N., Li Y. P., Flavell R.,
RA Feldmann K.,
RA "Full-length cDNA from Arabidopsis thaliana."
DI 01-MAR-2003 (TrEMBLrel. 20, Created)
DE EMBL: AY067231; AN64834.1;
DR InterPro: IPR001229; Jacalin_lectin.
DR Pfam: PF01419; Jacalin.
DR PROSITE: PS00601; NOS.
SQ SEQUENCE 458 AA: 50376 MW: 6D3F10FB31B83C5 CRC64:

Query Match 91.4%; Score 32; DB 10; Length 458;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 214 GRGDTP 219

RESULT 7
Q8YKQO PRELIMINARY: PRT; 456 AA.
ID Q8YKQO
AC Q8YKQO
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein A17243.
GN ALR7243.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC Plasmid pCC7120alpha.
NCBI_TaxID:103690;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-2595285; PubMed-11759840;
RA Kaneko I., Nakamura Y., Wolk C.P., Kuritz J., Sasamoto S.,
RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shirao S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2003).
DR EMBL: AF003600; BAB78327.1;
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank.
DR SMART: SM00248; ANK.
DR PROSITE: PS00088; ANK_REPEAT.
DR PROSITE: PS00297; ANK_REPEAT_REGION.
DR PROSITE: PS00300; SRP54.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 606 AA: 66738 MW: 54A8102A582282 CRC64:

Query Match 91.4%; Score 32; DB 16; Length 606;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 120 GRGDTP 125

RESULT 8
Q9DQD2 PRELIMINARY: PRT; 23 AA.
ID Q9DQD2
AC Q9DQD2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Enhancement of wound HEALING process.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID:9606;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE-95130623; PubMed-7829572;
RA Pierschbacher M.D., Poirak J.W., Craig W.S., Tsibulsky J.P.,
RA Sipes N.J., Harper J.R.;
RI J. Cell. Biochem. 56:150-154(1994).
RL [2]
SQ SEQUENCE 23 AA: 2268 MW: CE736997B97389 CRC64:

Query Match 88.6%; Score 31; DB 4; Length 23;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 1 GRGDTP 6

RESULT 9
Q9E2D2 PRELIMINARY: PRT; 86 AA.
ID Q9E2D2
AC Q9E2D2
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 9.1 kDa protein.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
NCBI_TaxID:382;
RN [1]
SQ SEQUENCE FROM N.A.

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RC STRAIN-RU11/001;  
 Muschler P.F.J., Foster C.;  
 "Isolation of mcp genes from *Sinorhizobium meliloti*."  
 Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  
 EMBL: AF298190; AAC37856.1; -.  
 DR Hypothetical protein.  
 KKW  
 SEQUENCE 86 AA; 9128 MW; 87035856B176DE2A CRC64;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 35 GRGSP 40

RESULT 10  
 Q8HUM8 PRELIMINARY: PRT: 185 AA.  
 AC Q8HUM8;  
 DI 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosomal protein small subunit 4 (Fragment).  
 GN RPS4.  
 OS Woodwardia fimbriata.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Filicophyta; Filicopsida; Filicales; Blechnaceae; Woodwardia.  
 OR NCBI\_TaxID=29664;  
 RX  
 SEQUENCE FROM N.A.  
 RA Cranfill R., Kato M.;  
 RT "Phylogenetics, Biogeography, and Classification of the woodwardioid  
 ferns (Blechnaceae)."  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AF533859; AAN34638.1; -.  
 KKW Chloroplast.  
 NON\_TER 1  
 SEQUENCE 185 AA; 20723 MW; D8795983F5283F9E CRC64;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 2 GRGSP 7

RESULT 11  
 Q8HUM7 PRELIMINARY: PRT: 185 AA.  
 AC Q8HUM7;  
 DI 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosomal protein small subunit 4 (Fragment).  
 GN RPS4.  
 OS Woodwardia fimbriata.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Filicophyta; Filicopsida; Filicales; Blechnaceae; Woodwardia.  
 OR NCBI\_TaxID=120727;  
 RX  
 SEQUENCE FROM N.A.  
 RA Cranfill R., Kato M.;  
 RT "Phylogenetics, Biogeography, and Classification of the woodwardioid  
 ferns (Blechnaceae)."  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AF533860; AAN34639.1; -.  
 KKW Chloroplast.

FI NON\_TER 1  
 SQ SEQUENCE 185 AA; 20699 MW; 9E9D177082010457 CRC64;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 2 GRGTP 7

RESULT 12  
 Q8HUM2 PRELIMINARY: PRT: 185 AA.  
 AC Q8HUM2;  
 DI 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosomal protein small subunit 4 (Fragment).  
 GN RPS4.  
 OS Woodwardia spinulosa.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Filicophyta; Filicopsida; Filicales; Blechnaceae; Woodwardia.  
 OR NCBI\_TaxID=120731;  
 RX  
 SEQUENCE FROM N.A.  
 RA Cranfill R., Kato M.;  
 RT "Phylogenetics, Biogeography, and Classification of the woodwardioid  
 ferns (Blechnaceae)."  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AF533866; AAN34645.1; -.  
 KKW Chloroplast.  
 NON\_TER 1  
 SEQUENCE 185 AA; 20723 MW; D8795983F5283F9E CRC64;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 2 GRGTP 7

RESULT 13  
 Q8HUM2 PRELIMINARY: PRT: 205 AA.  
 AC Q8HUM2;  
 DI 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein R02299.  
 GN R02299 GR SMC01349.  
 OS Sinorhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.  
 OR NCBI\_TaxID=382;  
 RX  
 SEQUENCE FROM N.A.  
 RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Gadiot T., Goffeau A., Kahn D., Kiss E., Leclaire V., Masuy D.,  
 RA Phil I., Portetelle D., Puchier A., Fumelle R., Ransperger D.,  
 RA Renard C., Trebault P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 Sinorhizobium meliloti strain 1021."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL: AL591790; CAC46878.1; -.  
 KKW Hypothetical protein; Complete proteome.

SQ SEQUENCE 208 AA; 21420 MW; A9222A3391FB522 CRC64;

Query Match 98.6%; Score 31; DB 16; Length 208;

Best Local Similarity 83.3%; Pred. No. 1.8e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

DB 122 GRGDP 127

RESULT 14

Q8N290

ID Q8N290 PRELIMINARY; PRC; 218 AA.

AC Q8N290;

DT 01-OCT-2002 (TRENBLrel. 22, Created;

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DI 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

DE Hypothetical protein FLJ33691.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI\_TaxID=9606;

OX 11

RN SEQUENCE FROM N.A.

RP TISSUE=Amalgam;

RC Ninomiya K., Katsushima M., Kanda K., Kondo H., Yokoi F., Kodaira H.,

RA Furuya T., Takafashi M., Kikawa R., Omura Y., Ake K., Kamihara K.,

RA Katsura N., Sato H., Tanikawa M., Yamazaki M., Sugiyama T., Ito K.,

RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Morakawa K.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami A.,

RA Suzuki Y., Sugano S., Nishihara K., Masuhara Y., Nishii K., Isono T.,

RT "NEDO human cDNA sequencing project";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AK090970; BAC03560.1;

KW Hypothetical protein.

SQ SEQUENCE 218 AA; 22892 MW; 65468419D52622DF CRC64;

Query Match 86.5%; Score 31; DB 16; Length 218;

Best Local Similarity 83.3%; Pred. No. 1.9e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

DB 4 GRGDP 9

RESULT 15

Q92PA3

ID Q92PA3 PRELIMINARY; PRC; 275 AA.

AC Q92PA3;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DI 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Hypothetical protein R01876.

GN R01876 OR SMC00134.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Sinorhizobium.

OC NCBI\_TaxID=382;

OX 11

RN SEQUENCE FROM N.A.

RP STRAIN=1021;

RX MEDLINE=21346507; PubMed=1141430;

RA Capela C., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

RA Bolstad P., Becker A., Boutry M., Cadieu F., Dreano S., Gloux S.,

RA Godrie T., Goffeau A., Kahu D., Kiss E., Lelaure V., Masny D.,

RA Pohl I., Portetelle D., Puhler A., Purnelle B., Ransperger D.,

RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallot F.,

RT "Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9677-9682(2001).

DR EMBL; AL591788; CAC46455.1;

DR InterPro: IPR000051; SAM\_bind.

DR InterPro: IPR001440; TPR.

DR Pfam: PF00515; TPR; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 275 AA; 29894 MW; BB53C158HC340CD CRC64;

Query Match 88.6%; Score 31; DB 16; Length 275;

Best Local Similarity 83.3%; Pred. No. 2.4e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

DB 58 GRGDP 63

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Web time : 35 secs